```
   1 ATGAGCCAGC CCAGGCCCCG CTACGTGGTA GACAGAGCCG CATACTCCCT
  51 TACCCTCTTC GACGATGAGT TTGAGAAGAA GGACCGGACA TACCCAGTGG
 101 GAGAGAAACT TCGCAATGCC TTCAGATGTT CCTCAGCCAA GATCAAAGCT
 151 GTGGTGTTTG GGCTGCTGCC TGTGCTCTCC TGGCTCCCCA AGTACAAGAT
 201 TAAAGACTAC ATCATTCCTG ACCTGCTCGG TGGACTCAGC GGGGGATCCA
 251 TCCAGGTCCC ACAAGGCATG GCATTTGCTC TGCTGGCCAA CCTTCCTGCA
 301 GTCAATGGCC TCTACTCCTC CTTCTTCCCC CTCCTGACCT ACTTCTTCCT
 351 GGGGGGTGTT CACCAGATGG TGCCAGGTAC CTTTGCCGTT ATCAGCATCC
 401 TGGTGGGTAA CATCTGTCTG CAGCTGGCCC CAGAGTCGAA ATTCCAGGTC
 451 TTCAACAATG CCACCAATGA GAGCTATGTG GACACAGCAG CCATGGAGGC
 501 TGAGAGGCTG CACGTGTCAG CTACGCTAGC CTGCCTCACC GCCATCATCC
 551 AGATGGGTCT GGGCTTCATG CAGTTTGGCT TTGTGGCCAT CTACCTCTCC
 601 GAGTCCTTCA TCCGGGGCTT CATGACGGCC GCCGGCCTGC AGATCCTGAT
 651 TTCGGTGCTC AAGTACATCT TCGGACTGAC CATCCCCTCC TACACAGGCC
 701 CAGGGTCCAT CGTCTTTACC TTCATTGACA TTTGCAAAAA CCTCCCCCAC
 751 ACCAACATCG CCTCGCTCAT CTTCGCTCTC ATCAGCGGTG CCTTCCTGGT
 801 GCTGGTGAAG GAGCTCAATG CTCGCTACAT GCACAAGATT CGCTTCCCCA
 851 TCCCTACAGA GATGATTGTG GTGGTGGTGG CAACAGCTAT CTCCGGGGGC
 901 TGTAAGATGC CCAAAAAGTA TCACATGCAG ATCGTGGGAG AAATCCAACG
 951 CGGGTTCCCC ACCCCGGTGT CGCCTGTGGT CTCACAGTGG AAGGACATGA
1001 TAGGCACAGC CTTCTCCCTA GCCATCGTGA GCTACGTCAT CAACCTGGCT
1051 ATGGGCCGGA CCCTGGCCAA CAAGCACGGC TACGACGTGG ATTCGAACCA
1101 GGAGATGATC GCTCTCGGCT GCAGCAACTT CTTTGGCTCC TTCTTTAAAA
1151 TTCATGTCAT TGCTGTGCG CTTTCTGTCA CTCTGGCTGT GGATGGAGCT
1201 GGAGGAAAAT CCCAGGTGGC CAGCCTGTGT GTGTCTCTGG TGGTGATGAT
1251 CACCATGCTG GTCCTGGGGA TCTATCTGTA TCCTCTCCCT AAGTCTGTGC
1301 TAGGAGCCCT GATCGCTGTC AATCTCAAGA ACTCCCTCAA GCAACTCACC
1351 GACCCCTACT ACCTGTGGAG GAAGAGCAAG CTGGACTGTT GCATCTGGGT
1401 AGTGAGCTTC CTCTCCTCCT TCTTCCTCAG CCTGCCCTAT GGTGTGGCAG
1451 TGGGTGTCGC CTTCTCCGTC CTGGTCGTGG TCTTCCAGAC TCAGTTTCGA
1501 AATGGCTATG CACTGGCCCA GGTCATGGAC ACTGACATTT ATGTGAATCC
1551 CAAGACCTAT AATAGGGCCC AGGATATCCA GGGGATTAAA ATCATCACGT
1601 ACTGCTCCCC TCTCTACTTT GCCAACTCAG AGATCTTCAG GCAAAAGGTC
1651 ATCGCCAAGA CTGTCTCCCT GCAGGAGCTG CAGCAGGACT TTGAGAATGC
1701 GCCCCCCACC GACCCCAACA ACAACCAGAC CCCGGCTAAC GGCACCAGCG
1751 TGTCCTATAT CACCTTCAGC CCTGACAGCT CCTCACCTGC CCAGAGTGAG
1801 CCACCAGCCT CCGCTGAGGC CCCCGGCGAG CCCAGTGACA TGCTGGCCAG
1851 CGTCCCACCC TTCGTCACCT TCCACACCCT CATCCTGGAC ATGAGTGGAG
1901 TCAGCTTCGT GGACTTGATG GGCATCAAGG CCCTGGCCAA GCTGAGCTCC
1951 ACCTATGGGA AGATCGGCGT GAAGGTCTTC TTGGTGAACA TCCATGCCCA
2001 GGTGTACAAT GACATTAGCC ATGGAGGCGT CTTTGAGGAT GGGAGTCTAG
2051 AATGCAAGCA CGTCTTTCCC AGCATACATG ACGCAGTCCT CTTTGCCCAG
2101 GCAAATGCTA GAGACGTGAC CCCAGGACAC AACTTCCAAG GGGCTCCAGG
2151 GGATGCTGAG CTCTCCTTGT ACGACTCAGA GGAGGACATT CGCAGCTACT
2201 GGGACTTAGA GCAGGAGATG TTCGGGAGCA TGTTTCACGC AGAGACCCTG
2251 ACCGCCCTGT GA
```

FEATURES:
Start Codon: 1
Stop Codon: 2260

HOMOLOGOUS PROTEINS:
Top BLAST Hits:

		Score	E
gb|AAF81911.1|AF279265_1	(AF279265) putative anion transpor...	476	e-133
gb|AAF71715.1|AF230376_1	(AF230376) prestin [Meriones ungui...	471	e-131
ref|NP_000432.1|	pendrin [Homo sapiens] >gi|11421915|ref|XP...	451	e-125
ref|NP_035997.1|	Pendred syndrome homolog (human); Pendred'...	448	e-124
ref|NP_062087.1|	Pendred syndrome homolog (human) [Rattus n...	447	e-124
ref|NP_067328.1|	down-regulated in adenoma [Mus musculus] >...	434	e-120
ref|NP_000102.1|	down-regulated in adenoma protein [Homo sa...	418	e-115
sp|O70531|DTD_RAT	SULFATE TRANSPORTER (DIASTROPHIC DYSPLASI...	365	1e-99
ref|NP_000103.1|	sulfate anion transporter 1; Diastrophic d...	362	1e-98
ref|NP_031911.1|	diastrophic dysplasia [Mus musculus] >gi|2...	357	4e-97

BLAST to dbEST:

	Score	E
gi|8630793 /dataset=dbest /taxon=960...	523	e-146

EXPRESSION INFORMATION FOR MODULATORY USE:
library source:
Expression information from BLAST dbEST hits:
gi\|8630793 Human head-neck

Expression information from PCR-based tissue screening panels:
Human fetal lung

```
  1 MSQPRPRYVV DRAAYSLTLF DDEFEKKDRT YPVGEKLRNA FRCSSAKIKA
 51 VVFGLLPVLS WLPKYKIKDY IIPDLLGGLS GGSIQVPQGM AFALLANLPA
101 VNGLYSSFFP LLTYFFLGGV HQMVPGTFAV ISILVGNICL QLAPESKFQV
151 FNNATNESYV DTAAMEAERL HVSATLACLT AIIQMGLGFM QFGFVAIYLS
201 ESFIRGFMTA AGLQILISVL KYIFGLTIPS YTGPGSIVFT FIDICKNLPH
251 TNIASLIFAL ISGAFLVLVK ELNARYMHKI RFPIPTEMIV VVVATAISGG
301 CKMPKKYHMQ IVGEIQRGFP TPVSPVVSQW KDMIGTAFSL AIVSYVINLA
351 MGRTLANKHG YDVDSNQEMI ALGCSNFFGS FFKIHVICCA LSVTLAVDGA
401 GGKSQVASLC VSLVVMITML VLGIYLYPLP KSVLGALIAV NLKNSLKQLT
451 DPYYLWRKSK LDCCIWVVSF LSSFFLSLPY GVAVGVAFSV LVVVFQTQFR
501 NGYALAQVMD TDIYVNPKTY NRAQDIQGIK IITYCSPLYF ANSEIFRQKV
551 IAKTVSLQEL QQDFENAPPT DPNNNQTPAN GTSVSYITFS PDSSSPAQSE
601 PPASAEAPGE PSDMLASVPP FVTFHTLILD MSGVSFVDLM GIKALAKLSS
651 TYGKIGVKVF LVNIHAQVYN DISHGGVFED GSLECKHVFP SIHDAVLFAQ
701 ANARDVTPGH NFQGAPGDAE LSLYDSEEDI RSYWDLEQEM FGSMFHAETL
751 TAL
```

FEATURES:
Functional domains and key regions:
[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 3
```
      1     153-156 NATN
      2     156-159 NESY
      3     580-583 NGTS
```

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 2
```
      1      45-47 SAK
      2     445-447 SLK
```

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 11
```
      1      18-21 TLFD
      2     158-161 SYVD
      3     240-243 TFID
      4     365-368 SNQE
      5     459-462 SKLD
      6     556-559 SLQE
      7     635-638 SFVD
      8     691-694 SIHD
      9     722-725 SLYD
     10     726-729 SEED
     11     732-735 SYWD
```

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

Number of matches: 2
```
      1       7-15 RYVVDRAAY
      2     447-454 KQLTDPYY
```

FIGURE 2, page 1 of 4

```
[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 10
        1       77-82   GGLSGG
        2       78-83   GLSGGS
        3       89-94   GMAFAL
        4      103-108  GLYSSF
        5      335-340  GTAFSL
        6      435-440  GALIAV
        7      481-486  GVAVGV
        8      485-490  GVAFSV
        9      581-586  GTSVSY
       10      681-686  GSLECK
```

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	51	71	0.893	Putative
2	82	102	1.020	Certain
3	107	127	1.729	Certain
4	130	150	1.497	Certain
5	186	206	1.723	Certain
6	228	248	1.517	Certain
7	256	276	1.898	Certain
8	288	308	1.252	Certain
9	338	358	1.568	Certain
10	383	403	1.304	Certain
11	412	432	2.345	Certain
12	469	489	1.997	Certain
13	619	639	1.146	Certain

FIGURE 2, page 2 of 4

BLAST Alignment to Top Hit:
>gb|AAF81911.1|AF279265_1 (AF279265) putative anion transporter 1 [Homo sapiens]
         Length = 738

 Score = 476 bits (1224), Expect = e-133
 Identities = 263/724 (36%), Positives = 428/724 (58%), Gaps = 36/724 (4%)
 Frame = +3

```
Query:   54  LFDDEFEEKDR--TYPVGEKLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLL 227
             L + EE R + P  + R   +CS A+ A++   LPVL WLP+Y ++D+++ DLL
Sbjct:   15  LNQEHLEELGRWGSAPRTHQWRTWLQCSRARAYALLLQHLPVLVWLPRYPVRDWLLGDLL 74

Query:  228  GGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVG 407
             GLS  +Q+PQG+A+ALLA LP V GLYSSF+P+  YF  G   +  GTFAV+S++VG
Sbjct:   75  SGLSVAIMQLPQGLAYALLAGLPPVFGLYSSFYPVFIYFLFGTSRHISVGTFAVMSVMVG 134

Query:  408  NICLQLAPESKFQVFNNATNESYVDTAAMEAERLHVSATLACLTAIIQMGLGFMQFGFVA 587
             ++  LAP+        A N+S ++  A +A R+ V++TL+ L  + + Q+GLG + FGFV
Sbjct:  135  SVTESLAPQ--------ALNDSMINETARDAARVQVASTLSVLVGLFQVGLGLIHFGFVV 186

Query:  588  IYLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICKNLPHTNIASL 767
             YLSE  +RG+ TAA +Q+ +S LKY+FGL + S++GP S+++T +++C  LP + + ++
Sbjct:  187  TYLSEPLVRGYTTAAAVQVFVSQLKYVFGLHLSSHSGPLSLIYTVLEVCWKLPQSKVGTV 246

Query:  768  IFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAISGGCKMPKKYHMQIVGEIQ 947
             + A ++G LV+VK LN +   ++ PIP E++ ++ AT IS G  +  ++ + +VG I
Sbjct:  247  VTAAVAGVVLVVVKLLNDKLQQQLPMPIPGELLTLIGATGISYGMGLKHRFEVDVVGNIP 306

Query:  948  RGFPTPVSPVVLQWKDMIGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIALGCSN 1127
             G   PV+P     + ++G+AF++A+V + I +++G+  A +HGY VDSNQE++ALG SN
Sbjct:  307  AGLVPPVAPNTQLFSKLVGSAFTIAVVGFAIAISLGKIFALRHGYRVDSNQELVALGLSN 366

Query: 1128  FFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGA 1307
              G F+   + C++S +L + GG SQVA    SL +++ ++ LG   + LPK+VL A
Sbjct:  367  LIGGIFQCFPVSCSMSRSLVQESTGGNSQVAGAISSLFILLIIVKLGELFHDLPKAVLAA 426

Query: 1308  LIAVNLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQ 1487
             +I VNLK  L+QL+D   LW+ ++  D  IW+V+F ++  L+L  G+ V V FS+L+VV +
Sbjct:  427  IIIVNLKGMLRQLSDMRSLWKANRADLLIWLVTFTATILLNLDLGLVVAVIFSLLLVVVR 486

Query: 1488  TQFRNGYALAQVMDTDIYVNPKTYNRAQDIQGIKIITYCSPLYFANSEIF---------- 1637
             TQ +   L QV DTDIY +    Y+ A++++G+K+   + +YFAN+E +
Sbjct:  487  TQMPHYSVLGQVPDTDIYRDVAEYSEAKEVRGVKVFRSSATVYFANAEFYSDALKQRCGV 546

Query: 1638  --------RQKVIAK--TVSLQELQQDFE-NAPPTDPNNNQTPAN-GTSVSYI------- 1760
                     ++K++ K   + L++LQ++ +    P         N  TS+ +
Sbjct:  547  DVDFLISQKKKLLKKQEQLKLKQLQKEEKLRKQAASPKGASVSINVNTSLEDMRSNNVED 606

Query: 1761  ------TFSPDSSSPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGI 1925
                   S D   A +    ++AP + S + A  P  FH+LILD+ +SFVD + +
Sbjct:  607  CKMMQVSSGDKMEDATANGQEDSKAP-DGSTLKALGLPQPDFHSLILDLGALSFVDTVCL 665

Query: 1926  KALAKLSSTYGKIGVKVFLVNIHAQVYNDISHGGVFEDGSLECKHVFPSIHDAVLFAQAN 2105
             K+L +  + +I V+V++  H+ V + +  G  F D S+ KH+F S+HDAV FA +
Sbjct:  666  KSLKNIFHDFREIEVEVYMAACHSPVVSQLEAGHFF-DASITKKHLFASVHDAVTFALQH 724

Query: 2106  ARDV 2117
             R V
Sbjct:  725  PRPV 728
```

```
Hmmer search results (Pfam):
Model      Description                                          Score    E-value  N
PF00916    Sulfate transporter family                          254.5    1.5e-72  1
PF00189    Ribosomal protein S3, C-terminal domain.              3.3           8  1

Parsed for domains:
Model      Domain   seq-f seq-t     hmm-f hmm-t      score  E-value
PF00916    1/1       187   497 ..       1   328 []   254.5  1.5e-72
PF00189    1/1       651   661 ..      79    89 .]     3.3        8
```

```
   1 CTGGGTTCCT ATGTGGGGAG GTCATGCTCC CCACTCATTG AGCCCCCCCA
  51 GGCAAACCAC CTGGACAGCC AGACCCATGC AGACTCTGGA GCAGGTGGAG
 101 AGGAAGAGTG AGACCACCCC GCCTCACGGG CGGTGAAGGG CCGGCAGCCT
 151 CTGAATAGTC TCTGCTAGGA GGTAGAAAGC ACCCTCCCAT CTTAATCATA
 201 GTAATCATCG CCACTACCAT TTACTGGGTG CCTATAAAAG GCCAGCCTCT
 251 TCATACACAT GATCTCACTG AATCCTCATA GCATCTGCCT GCGACTGTTA
 301 TTATCCCCAT TTACAGATGA AGAAACTGAA TCTTTGAACC CAGGTCATCT
 351 GGCTCTCAAA CTTGTGCTGT TTTCCCTAAG CCACCGGTC TCTCATTTCT
 401 CCCACTGAAA TGTCTCACAT GCCATTGCCC TTACTCATTT CTGCCCATGT
 451 CTCCTCCAAA ACACCATTTA TCAATTCGCT CAACAAGTAT GTGTTGAGTA
 501 CACACTAAGG GCCAGGCGAG GGGCTGGGCA CAGGCGCTGG GGGTAGGTTC
 551 ATTCTCCCAC CTTCGCTTCT GCTGGGTATC ACCTGTGGGG TCTTGCCGGG
 601 CATCCCACCC TCACCTGTAG TTCAAGTGGA CCTTGGGATC CCAAGACCAA
 651 ATGAATGGAA TGCACCAGCC CAGCCTTCAC CAACTTGAGC ACAATCTTAT
 701 TCATAATAGA AACTCACATT TGCATCACAC TTTACATTTT ACACAACCCC
 751 TTCTTATCCA TTAACTCATT TGATCTTCAC AACAACCCTG TGAGATATGT
 801 CTGTTACTCC CACTTTAGTG ATACAGAATC TGAGGTTTGA AAAGTAATGC
 851 TGACCATTCT GCCTCATTAA TAAAAGCAGG ATTAACCCAG GCTCCTGGAC
 901 CCTTCCACAA AAGGCATTAA GCAACCTGCT CCCCTCTGAC AACCTCCCCT
 951 GTCACCCAGG CTCTCCTCTG GGAAGTTGGG GGCATCTCTA GCCCCCAAGT
1001 AGTTACTCAT TTTCAACCCC ATCTCAAATC TTTTGCCAAA CTGGCCACAG
1051 CCACCCCACA CTCCCCACCT CCCAGATACA AATCCTCACT CTAAGCCTTC
1101 CCCATCTCTT TCTTCTCTGT CCTTCTTTCT CTGTGGTCCT CTGAGCAACT
1151 TCTCCCAGCT CTGGGAGGTA GAGGGGAGGT GGGAGACCCA GTAATTGGAA
1201 GAGGGAGGGG GAAAGGTTCC TACAGGGAAC TCCTCCGGGC CTCAGGGGCC
1251 CTGGCACTCA GCTCTGCCCA TCTCAGCTCC TGGAACGTCA GCCAGGTTGC
1301 GCAAAAAGTG AGGAGGAGAG GAGCGGCAGT ACACAAGGGT GGGGGAAAGA
1351 TTAGGCACAG GAAGCCGTGG GAGAGAGAGC CGGCAGGTGG ACCATCCTGG
1401 TTTCCCCACA CACACCATTG TCCCCCTGGG AAACCTGTTG GTGAAGTTCT
1451 AGATGTCTTA TCCAAGAAGG GTCCTCTTGA GGTCATCTCA GCTATCCCCC
1501 TGCCTCTAGG CAAGCTGTTT TCTGTTTCTT CCAAGCTGAC TGGCTGAATG
1551 GTAGGAGCCT TTCTGCCAGG GAAACTAAGG TCTGGGAAGG GAGTATGGCT
1601 TGTGGGGACA CCAGGGGTCA GGGGAGGGGA GGGTCCACCT GCTGAATCAA
1651 GTGGGGCCTC CTGCCCTCGT GATTCCCCTT TGCCTGGTGC TCAGTGGGGG
1701 TGATGGTGAC GCCACAGGTG TGGAGTGCCA GCCACGTGCT GAGCGCCAAG
1751 CAAAACAGCC AGGGTGAGTC TATGCATCAT CAGTGCCTGG GAAGGAAGGC
1801 CACTGCGAGC AGGGAGTCTG ACGGAAAAAC TTGACAGAGG GAAGGGAGGC
1851 ACCTTGCTTT ATCGGGGCGG GGAAGGCCAG AATAAAACTC TGCTACTGCA
1901 AGGACCAGAG AGAGAAGGCC TGGGCTGGCA CTAGGGAGGG ATGTTCCCTC
1951 ACCCTCCCCT CCTCTGCTTC TCCCAAAGCT TGTAAATGCC CCAGATATGA
2001 GCCAGCCCAG GCCCCGCTAC GTGGTAGACA GAGCCGCATA CTCCCTTACC
2051 CTCTTCGACG ATGAGTTTGA GAAGAAGGAC CGGACATACC CAGTGGGAGA
2101 GAAACTTCGC AATGCCTTCA GGTAACTGGT CCAGAGCCCA GACTTCTGCC
2151 TCCTCTGCTC CCTACCAAAA TCCTTTCTGC ACCAGGACAC GGCTTCTGCA
2201 CTGGTATCCC TAAGATGGGG TTAAGGGAAG CCCTGGGGAA GTGAGGTTCT
2251 GAATGATGAA TTTAAGATCC TACAACCTCA TCTGTACTGA GACCCCCAGG
2301 GAGGATGGGG AGCAGGAGCA AGAACCATCC AGAAGGGTTA TATGGCATTC
2351 CCAAACCCCT GCATGGCATC TCCCATATTC TCAATTCACC CGGGTCTCTC
2401 TGGGTTTGTT AAGGCATGGT AGATGAGCAT CTACGTTATG GAGGGGTGGG
2451 GAGCATCAGA GCCCTTACTC CATGCCCTGT TCCCTCCTTA CAAAAAATAC
2501 CTGAAGTTAC CATCACCCCA GGTTCTTTGT CCTTTCCCTC CCGGATGTTC
2551 CTTCCTCCAC TTGGTCCAGA GAATGCCAAA AGGAGGCCCT AAATTTCTGA
2601 ACTTTCCTGA GGGGACCTAC CAGGGTGTAG TCCTACCAGC GCCCAGGGTC
2651 TTTCCACTCT CATCTCCCTG GAAATGCGAT GGTGGGTATG AAACCTTGTC
2701 CCTAAGTAGG CGCTACACAA GGTGATCCAT ACCCACACCC CAGGAGGCTG
2751 GGGCTGCGGG TGTCACCCTC CCCATTCCCA GACTCCTGGC AGACCTCCTC
2801 TGGCCCAGCT ATAGGCCAAC TCACTCTCCC TCACTCCCTT GGGGAAACGG
2851 CTGATTCAGT TACCTGGATT GAGGTCACTG GCAATGGCTG AAGTGGAGAC
2901 GCAGGTGGAA CTGGTTCAGG CCGGGGGAAT CACCCACTTG AGTTTGTACT
2951 AAAAGCCCCA GCCCAGCCCT GTTTCTCTTG GGAGGCTCCA TTTCTGCCCA
3001 GTTACAGTCT GTCCTCACAG CTGTGCTCCT CAGACAGGTG GTCTCTGCCA
3051 GTCTTTGTGC CCAAGACTTT AGGGCACAAA GTCTGAGGAT GAGAAGATCT
3101 GCTATTGTCC TAAAAGATTA GGATAATGAA AGCTGTAAAG GGATATAGCA
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FIGURE 3, page 1 of 20

```
3151 AACTAACAAT TCCTATGATA CTGGCATGAG AGCCTTGAAC AGTGCCTGGC
3201 ATAGAGAAGG TGCACCAATA AATATTTGTT TCATGAATGA ATGAATGAAT
3251 GAATGCTAG AAAGCTAATC CCTCTCAGCC TCTGTTTCCA GTTCTTCTTT
3301 CAAGCTTCAG ATTGCTTTGC CCAACATACA GCAGACTTGC AAGTAAGGTT
3351 GGGCATGGAC TAGCCCTCAA ATGAGTTGTT TTTCTTTCCC TAGCCAGCTC
3401 TCTATTCATA AGTCCGGCTT TCTCTGCCAC AAACAGACCT GATGGAGCCC
3451 CTGCAGGGCT GGTTCTCTCT TCAAGCAAGG CTTTAGAGTT GCATTAAGCA
3501 ATTTATCCCC CGTCCACCTC CCCTTCCAGC ATCCCAGGGA TGGCAGAGGC
3551 ACCCATGAGC CCCAGAAGGG ACAGGGGGTA AGATATTGAT GATGATGCTT
3601 TTTCTTGGAG TGTTAGTTGG AAGAGAAAAT CTGCCCAGAC TTTCCAAGGT
3651 ACAAAGCATT GTCTTTGTTG GTTTCAGTCT TGGGTGACAT CCAGGGGACC
3701 GAGTGTCAGG GAAACTATTG TTGAGCAAGA GCAAAGAGCA GGAATTGGTG
3751 CTGGGCAGGA AAGGAAGCCT CATCAGAGCA GGCCAGTGAG TCACCAAATG
3801 GGCCCTAAGT ATTTGAGTTC CCTCAACTGG GAGAAGGAAA GCAAATGCCC
3851 CTCACCCACT TCCAGTCATC AATCCACCGG CTGTCACCCT TGAGTTTGTA
3901 AGCCCTTGTT CCTACCGCTC CTGAGTTTCT ATGAAAGGAC CTTGAGGTGT
3951 TCAACAAACA GGGAAGGGAT CAACTCTCCC CACCCTGCGT TGACCAATGA
4001 ATTCTTCCCT CCTCTGCTGC CCAGTGAATT AACAGGAGAA AGAACTCCGG
4051 TATTGGAGTT ACCACACATA AAGGATAGTG AGTCAGCAGA GTGCACCCTG
4101 CAGGAACAAT AGAGCCTTCC TTTTCAAGGA AGTTCTAAGA AAAATGGCAG
4151 CAGGCAGGCC CCACTCGGGT GTATTCACTC ATTCATTTAT TCAACAAATA
4201 TTTACTAAGT GCCCCTGTGC AAGGCTCGAG GTGTACAAAG ATGAACAGGA
4251 GAGCTAGACT TCTTGCCATG CGTGGTGGGG TTTGCTGCCT AGTGGGAGAG
4301 ACAGACAAAA AGCAAGGAAT GCACACACAG GATGCACACA CAGCGGCAGG
4351 AACCAAGGTG CAGTTACCCA GGCCTGGGAT CAGACAGACA GGACTCAGAG
4401 GAGACTTTCC CAGAGAAAAG CCATCTGAGC CAAGGGATGG ATCTGATACC
4451 TCCGAAGGCT GAGCCACCAT AACACTCATA CCTTTAAGCC AAGTCTTATA
4501 AACTCCCCAG GTAAGCAGCT GGCAGTCAGA AGACCTCCAG CTAATGCCCA
4551 GGACAAGTTG ATGAGCTCTC AAGAAAAAGT TCCTGCCTTT TCTTCTCAAT
4601 ATCCCTGGCA CACAGTTCAG TGAATTTTGA ATGAACCAAT GAATGAAATG
4651 AGCAGGATAT GATAATCCCT CTCCAACACG GAATGTCCAA GCCATGCAGA
4701 GCCGACTGGA AATTTTCCCC GTTCCCTTCC AGATGTTCCT CAGCCAAGAT
4751 CAAAGCTGTG GTGTTTGGGC TGCTGCCTGT GCTCTCCTGG CTCCCCAAGT
4801 ACAAGATTAA AGACTACATC ATTCCTGACC TGCTCGGTGG ACTCAGCGGG
4851 GGATCCATCC AGGTCCCACA AGGTGAAGGG GCTCCTTCAG CCAGGCCTGG
4901 ATTGCCACTC CCCTCACCAT TCCTCTCCTC ATCCCCACTC CATCCCTCTG
4951 TGATCCCCAT AAGCTAGTCA TGCTGCTGAG CTTCAGTCTC GTTGTCCTCT
5001 GCAGGCATGG CATTTGCTCT GCTGGCCAAC CTTCCTGCAG TCAATGGCCT
5051 CTACTCCTCC TTCTTCCCCC TCCTGACCTA CTTCTTCCTG GGGGGTGTTC
5101 ACCAGATGGT GCCAGGTAAG GCCTCTCCCC TCTGGGCAGG CAGGATGACC
5151 CAGACCACAA GGATGGGAGG TGTGGCAAAG GGGCCTCGGG AGATTTTCCA
5201 TCTGCATTCT CCTGGAGTTG TTCCTGGTCA GTCCTAGGGG AATGGTCACT
5251 GTGAATGTCA TTTCCAGGTC CTCGGTGACC TTGGAGAAAC CACTGAGCCT
5301 CTTTGAGTTC AGTTAGCATT ACCTGTTCCA TCTTCCTCCT AGGAATGAGA
5351 GGAAGACTTA GCAGAACAAG ATATACCATA TGCTATAACA TGCTTAAACA
5401 GATGTGAGAA ATCACCATCT AACTCCCTGG TTGGTCCCAG CCGGCCACTA
5451 CAGGGACATT TGGACTTCTC TGGTGCTAAG TGAGATGGAG GAAAGCCTGG
5501 TCACAAGGGC TGGTTTCTGG TTCAGGCTCT GCTTATATTT CTTATTTCTG
5551 AGTTCATTTT CTCACGTGTC CTGTATGACA ATATTGACCA TTGGGGTAAA
5601 AGCACCTTGA AAAGCATAGA TCATGGTTAG AGTGAGTGGT TGTTATTATT
5651 GTGTTGGAGA AGAGCCTTGG AGGTGCAGGG ATCCATCCCC CTGGGGTCGG
5701 GAAGCATTCC TGGGCCCCTT TCTGGTTTCC ATCGGTGTGG TTCAAACCTC
5751 TGATTTTTGC TGGCTGGGTG GGGCACCACA GGTACCTTTG CCGTTATCAG
5801 CATCCTGGTG GGTAACATCT GTCTGCAGCT GGCCCCAGAG TCGAAATTCC
5851 AGGTCTTCAA CAATGCCACC AATGAGAGCT ATGTGGACAC AGCAGCCATG
5901 GAGGCTGAGA GGCTGCACGT GTCAGCTACG CTAGCCTGCC TCACTGCCAT
5951 CATCCAGGTG AGGGGGCAGC CCCCAACCCT GCTAGAAGGG CATCAGACCA
6001 CCCTGCCCCT CCCTCAAAGC CTTAGCTTTG ATGCTAAATC TGATTTAGGG
6051 GGCTGGGTGT GGAGGCTCAT GCCTGTAATC CCAGCACTTT GGGAGGCTGA
6101 GGAGGGTGGA TCACTTGAGG TCAGGAGTTT GAGACCACCT TGACCAACGT
6151 GATGAAACCC CATCTCTACC AAAAATACAA AAATAATCCA GGCTTGGTAG
6201 TATGCGCCTG TAGTCCCACC TACTCAGGAG GCTGAGGCAG GAGAATCACT
6251 TGAATCCGGG AGGCAGAGGT TGCAGTGAGC TGAGATCGCG CCACTGCACT
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FIGURE 3, page 2 of 20

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6301 CCAGCCTGGG TGACAGAGCG AGACTCCGTC TCAAAAAAAA AAAAAAAAAA
6351 AAAAAAAAAA CCCAAGTTAG GGCTCACCTC CTCCCTCCTC CCCATCCCAG
6401 GGCTAAAGTG AACCTTGAAA ATTAACAGTA TCTCCTCATC TGCATGTAGC
6451 AGGACCATAC AAAAAAACAA CAGCTGTACC TGGTTAAACT GTCCTGAGCT
6501 TTAAACCTGT AAAAGACTCA CAGCCTCTCT CCATTATCCC GTGGAGAAAC
6551 CCAACTCTCT GCCAGCATAG TCTTGCAGAC TGCTAATTTT CTCTAACATC
6601 CCTCACTCCG CTCCAGCCTC CTCTGCTCCA AGCCACAGCA GCAGTTGCAC
6651 AACATAAATT GAGCTTCTGC AAATGGTTGC AAAGGATTCT GCTAGGTTTT
6701 ATGAAGGGAA GCACAACATG ACAGAATGCA AGAGCAAAAC ACAGTCCCAG
6751 AGAGCGCCTT TTCATTCACT CATTCATTCG GTTTTGTGCC AAGAACTAGG
6801 CTAAACCCTG GGATACAAAG ATAAGTAAGA AAGAGGTCCA ATTCACAAGT
6851 TGCTCACAGC CCAGCAGAGG AAGGAGCCAT GTCAACAGAT AAATTTGTAT
6901 GCAGTGAGAT AAGCAGCAAA GTAGAGCCAT GTACAAAGAC TGTAGGGACA
6951 CAGAGCAGAG TCACGGAGGA CCTCAAAGAG GAGGTGACAC TCCACCTCTC
7001 TTAAAGGATG AGAACTTAAC CAGGAACAAG GTATACAGAG GATGGTCCAG
7051 GCAGAAGGGA ACAGTGCCTA AAAACACTGA GGCCTGAGAG AGTGTGATCT
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7151 AGAGGATGGA AAAGTAGGCA GGAGCCAGAC AATGAGATCT GGGGTCTGTT
7201 CTCTGACAGC GACTTTGGGT CTGATTGGCA GTTTATAAGG ATCGTTTGGG
7251 CTACACAATG ATGAGTGGGA GGTGGATTAG AATCAAGGCA GGGGACCTGT
7301 TGGGAGACTC TGCAGAGGCC CAGGCAGGAA TAATGCAGGC GAAGACCAGG
7351 TAGAGAAAGA GATGGGGCTG GACTTGAAAA GAATGTTTTA CCAGGAGCTT
7401 GGTGATAGAC TGGATGTGGG AGGTAAGGGA GGATGACTCT CAAGTTTTTG
7451 GTTGGGCAAC CAGGTTAATG ATGGTGTCAT TTACTGAGAG AGAAACACT
7501 GGGGGAGGAC TAGACTTATT TTACAGATAA GCCAAAGCCA GAGAGGTGAT
7551 GTGACAGAAA GGCCCATGCT CTAAAGGAGC TGAAGGTCTG ATGGCAGCCA
7601 TGTAGAGCAC AGTGAAGGGC AGGTGAAGGT CACAGATGGT CCAATTCCCT
7651 CAAGCTACTG CTACGCTAGG ACTGCACGGA GCTCCAGACC TGCGTGTGTG
7701 TGGGGCGGGT CGTTGGAACT GCTGAACCAC ATTGGTCTTC CGCCACCAAC
7751 CACCCTTTTC CTCCTCTCAG ATGGGTCTGG GCTTCATGCA GTTTGGCTTT
7801 GTGGCCATCT ACCTCTCCGA GTCCTTCATC CGGGGCTTCA TGACGGCCGC
7851 CGGCCTGCAG ATCCTGATTT CGGTGCTCAA GTACATCTTC GGACTGACCA
7901 TCCCCTCCTA CACAGGCCCA GGGTCCATCG TCTTTGTGAG TCTGGGGATG
7951 CACCCCTGCC ATTGGAGCAA GGCTCCAGCA GACACATGAG GAGGATGTAC
8001 TGTTTTAAGA TGTCGTGAGC TCCTCATTGC AAGGGCTGGC TTAGCTGTTG
8051 TTCAGAGAGG ATTCTGAGGG GGTTTCTGTC TTGGGAGGGT CAAAGTCATG
8101 ACTCACAGGA GTTCTTGGTA GTTAATACCT GCAGAAAAGA GCTGTACATT
8151 CTCCGCCAGT TCCCCATTCT AGTGCCTCAA CCCCTCCCTG CCTGGAAAGT
8201 CCTGCCTTAT GTCTAATCTC CATCCCTCCT CCTTCAGCCC AAACTCTTCT
8251 AAAGAAAAAG AAAGCATTCC TTTTCTAGCA CAAGTTCCCC ATGTGCCTTT
8301 TGGGAAAGGG CGGTGGGCGA CGGGACAGGG TTCCTGATCA GGGTTTTAAT
8351 TCTGTCTTGG TGTGCCTCCA TTAGCTTTGA TGGCATCCCT TCCCTGGGTC
8401 AGACACCCAA AGGTGGGGTA TTATGGGAAG AAGGGGTGGG AGCCTGTGAG
8451 CATGATGCTC TTTCCCCCAG ACCTTCATTG ACATTTGCAA AAACCTCCCC
8501 CACACCAACA TCGCCTCGCT CATCTTCGCT CTCATCAGCG GTGCCTTCCT
8551 GGTGCTGGTG AAGGAGCTCA ATGCTCGCTA CATGCACAAG ATTCGCTTCC
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8751 CATCCCCCGT ATGTGGCGTT TCCTCTCTTT CTACTGCTCT AATAATTCCC
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9151 CTGAGAAGGG CCGCACAACC AGCCAATGTA GGCTATTTTA TGAGAAATGA
9201 GTCTTAACTG CCACACTCCC CTTATAAATC TCATTCAACT GATGCTGTTA
9251 AACAAAGCCT CTCTGAACAG CCGCTTGCTG GCTCTTTGCC TTGCTCTAAT
9301 GCATTGGTTC TTTGTCCATG TAGAAAGGGA ACTATTAGGT TCAACCAGAT
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9401 AGGGGTGACG CTTGTCCTGC AGGGTTGGAA CAGGCAAGGG AGGGAAGACC
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 9451 ACATAGCACC AAAGGTCTAG GGGTCTGTGG ACTCGTGAGC ATACAGGGTT
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 9701 CTGTGGGCTG GTGAAGGACT TGGCTGCCCT CCCCACTCAC ACCCTTGGGT
 9751 TCTGCCTCCT TCCTGGCTCC TCGGCAGGTT CCCCACCCCG GTGTCGCCTG
 9801 TGGTCTCACA GTGGAAGGAC ATGATAGGCA CAGCCTTCTC CCTAGCCATC
 9851 GTGAGCTACG TCATCAACCT GGCTATGGGC CGGACCCTGG CCAACAAGCA
 9901 CGGCTACGAC GTGGATTCGA ACCAGGTAGC TCTGGCCACC CCCGGCAGGA
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11801 GGTGAGACTC ATGCAGTCAT GGTTGCGTCA AACGCTGGTT CCGAGGATTA
11851 AATGAGATCC CAGTGGGAAA ACACCGCATG AGCGCAAACA TTCTGCAAAC
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12001 AAGCCCCACC ATAACCTATG GGAGAGGATT TACTAAACTT TCTTAACGGT
12051 GATGAAACCA AGGCTCAGAA TGGTTAAGTA AATTGTCAAA GGCCACAGAG
12101 GTAGGGAGTG GTAGAGTCTG GATTAAAACT CCAAGTCCTG GACTCCAGAC
12151 CTCTAGGCTG TACTGTCTCA TAGGGAAGGC AGTCTCACCC ACCTAGGGCA
12201 GAGAAGAAAA TCCTTAAAGC CAGAGAAGTG AGTGGCTCAT CTGTGGTCAC
12251 CCAGAGAGAC AGTGATGAGG ACAGGGAGAA AAATTATACC TCAGTTCCCA
12301 GCCCAAGGAT CTGCTTTGAC CATAACCCAA CAAGCCCCCG CTATGGTGGT
12351 ATTTCCTTAG GTTCATATGG CGGCTTTTGT TTCCATTTGA TCTTCACAGC
12401 AATTCTCTAC AGGAATCTGG GCAGATTTAT TTCCTTTAGA GGAATTTCCA
12451 GGTCTTAAAA TCTATAGGGG GCAACTATCA AAACTTCACC CAATGTTGCC
12501 CCCTACCCAC ACACAAAACC AGGCCCCCAG CCGATCAGAA AGCACTGCTG
12551 AGCTCCTGTC AGGGCCCACG CAGCTCGCTG TGAGACAGAG AGAGGGAACT
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13451 TGATAGCTTC CGCCCTCCTA GGCCCACAGT CGGTTCCCTG GGCCAGCCCG
13501 CAAAGGGCTT CCATGCCACG GCCTGGCTTA GTCCACTGTA CCTTCCACCT
13551 CTGGGCCTGG CACTGGAGGT GCTGCCAGGC CCAAAGAGAG CCCAACCCAG
13601 CCAGGACTGT GGGCACAGTC TGGGCTGTTT GACTTCCCAT ATCTTGAAAA
13651 CCCCAGAGAA AGCCAGCATA CTCTTGCTGG GGATGGCTGG GGAGAGGGCA
13701 GTGGCAGAGA AAGGAGGGCA AGGGCAGGTG GTGAGATTCA ACATCCTTCC
13751 AAAGACATTG CCAGAACCCC AAACCAAATG GGACCCCACC CCAGGAGAGC
13801 GCCAGGGTGG AAGACAGAAG CTGTGTTCTA CACACTGGGA GTATTACAGA
13851 GAAGGGGTCT TGGCCAAGGC AGGGAGTACG CTGAATGTTG GGGGAATCCT
13901 ATCTTCTCTT CTTGAGAACT CAGAACAAGG AAATGATGAC TTCAGGGCGA
13951 CTCCCACCAC TTCTCCCACC ACTTCTCTCC CCTGCCCTGT GGTCTGGGAG
14001 CTATGTCAAG GACCTGCCTG TCATCCTCAT AGTTATAGGA GGCCACAGGC
14051 CACCAGACAT GTGTCTCCAG TGCAAAAAGA CAGACACAGC AAGTCTGGGG
14101 GTGAGGACAG GACCCCATCC TACCTTGGCT CTGCCCCCGC CCCAGCAGGG
14151 GCACCCTTCC AGGCCCATGT GCCATTAGCA TTCTCTTATG TTTTTCTCTT
14201 CCTGCTTCAT CCAGTCGAAA TGGCTATGCA CTGGCCCAGG TCATGGACAC
14251 TGACATTTAT GTGAATCCCA AGACCTATAA TAGGGTAGGT AATTCAAGCT
14301 TATGACCTCC TTCTTTTGCT CTGCACCACC CCAAGAAGAG GTTGCTTTTT
14351 AAAGCCAATA AAGACATTTC TGCAACTTGA GCTCAGTCTC CCTGTCACAG
14401 GCCCAGGATA TCCAGGGGAT TAAAATCATC ACGTACTGCT CCCCTCTCTA
14451 CTTTGCCAAC TCAGAGATCT TCAGGCAAAA GGTCATCGCC AAGGTAAGGC
14501 TCAGTCCCTG GCGACCAGAG GCTCTGGACA GAGAGTGGCC GGAAAATGGA
14551 AGCAGAAGGG CGGTGGGAGC TGAGAATAGG CCACTCCCAT AGAGGGTGGA
14601 GGTCAAGATT GCTGTTGGCT CTCTCCCTGC AGACAGGCAT GGACCCCCAG
14651 AAAGTATTAC TAGCCAAGCA AAAATACCTC AAGAAGCAGG AGAAGCGGAG
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14851 GGCAAAGACA GAAAGTCTCT GGGAACACTG CCTGGTGGCC GCTGGGCATT
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15301 ATGGCCCATG GACTTTTGAA CAACCCAGAG GGGGAACAGC AGTGAATTTC
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15401 GTAATCCTTG TAATCCCAGC ACTTTAGGAG GCCGAGATGG GAGAATCACT
15451 CTCATGAGTT CAGGAGTTCG AGACCAGCCT GCCCAACGTG GCGAAACGCT
15501 GTCTCTACTA AAAATACACA AAAATTAGCC AGGCGTGGTG GTGGGCACCT
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15601 GAGGCAGAGG TTGCAGTGAG CCGAGATAGT GCCACTGCAC TCCAGCCTAG
15651 GCAACAGAGG GAGACTCTGT CTCAAGAAAT AAAGGAGCTC AGTGTCCCCG
15701 GAGGGGCTTT CTCCCAGAGA GAGTGGGCTT GAGGCTTCAG TGCCTCTCTT
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15751 GGCTGGGTCC TCTGACTTTG TCTGGGTTGT AGGAGACCAA GTTTGCAGGC
15801 CCTGCCTAAG AAAGGGCTTT GGGAGAGGCC TCTCTGGTGG AGCTTTCAGG
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15901 CCATGCCCCT GCTTCAGTCA CAGCAAGGTC TGGCTCAGTC TGGTGGTCCC
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16351 GAAGCTGAGG GAGGAAGCTC ACTGGGGAGA CTAACAGCTC CTAGGAATCC
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16451 CAGACGGCCC ATGACAATGA GTGGCGGGAC AAGTCTACCA GAGTTTCAGG
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16551 CCATCAGGAA CCCACCCAGG TTCTCTGAGG AGGGTCCAGT TTGGCTCCTG
16601 GTTCATGATC TGCTGCCCTT GTCCCTCATT CACCAGCCAC CCTAGGACAG
16651 GAGAAGAAAT AATACCAGTG CCCCACACCA TCAGGCCAAA CAGAGAGCCC
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16751 CGCCAATGGC GGGAGTCAGC AAACCTCAGA GCTGGCTCAG ATAGAGGCAA
16801 GCCAGGGGAA CAATGGGCAC AGAGAGTGTT CGGACTGCCT TCACCATCAA
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16901 TTAGCCAGGA TCTGGAGTCC AGGCCAGCCT TGGCTGAAGC TCTAGACTCC
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17751 AGCACCCAGC TATCCCCCAC AAGCTGCTGC CTGCTCATAA AAGCTTCAGG
17801 TACAAGTCCA AAGAGACTGG TCAGATTGCA TAAACATCCT AGGGGCCTTA
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17951 TTTATCTCTC AAGGGATCTA TTTCTACCTA TGTAAAACGA GAGGGTTGAC
18001 TAGATGGATT TGGGGATCCT CTCCCAATCA GAAACTCTGT GAATCGATAT
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18101 AGTTTTGTAG GCATACAGCC TCCAAAGGGT GCATATACAC AGCCTCAAGG
18151 ACGTGGCCAC AGGGCAGCAG ACATTTACAT GACTAGCATG TACGCAAAGT
18201 GCAGAGATGT GGGAGCAAGT GCACACAGAC ACACAGGAGA ATGTGAAGGG
18251 GCACATACAC ACACACCCAG CTCCCTGCAC TGGGTCAGAC CCCCTCCAGC
18301 AGGGCTGCAG TTCCCAAGCT CCGCATGGCC ACGTTCGGGG AGAGAATCTG
18351 CAGTGGCAAT GACCTGCTAT GATATGTTCT GGAGTTAGAA GCAGTGGATT
18401 CTCCCCAACC TCACTGGACA CCCCCCTTAGG AAACCATCTC TAGGATTAAG
18451 AGTAATCCAC ACAAACTTCC AATGCCACAC ATTGGAAGTT GCTGGAAAGG
18501 TCTGGGAAAA CAAGAGGAAG GATGGGTCCT TGGGGGATAG AACTGGCAGC
18551 GGCCTCTTCA AGGATGGCTT AGGCTTTTCC ACTCGAATCA CCACAAAGTA
18601 CTGACTCCCT AAATCAAACT GCTTCCTTCT GCTCTGGGTT GAAACTTCAG
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18701 CCAATGCCAT GGCCCTCAGA TACAGCAAGA GCTGGGACCT CAGGCCTCTC
18751 CCATCCCTGC TCTGGTCTCA CTATCTTCCC CACCCCCAGC TCCAATCCAC
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18851 TACAATGACA TTAGCCATGG AGGCGTCTTT GAGGATGGGA GTCTAGAATG
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18951 ATGCTAGAGA CGTGACCCCA GGACACAACT TCCAAGGGGT AAGGTTCTTG
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19601 CAGTCATCTC TAGCCCTCAG GGTCCCCTCC CAGCTCAGCT CCTGCCCTTG
19651 GCCTCCCAAG ACTCTTGTTG TGCCCCAGCC CTGGGTAAAA ACCTCCCCTG
19701 CCCTCTGTGG GTCATAAGAA AGGCTTTTCT GGCCCTAGAG CAATGATTTG
19751 CTCTTTGCCT TAAGAGACTG ATGAAGGTGA AACCATCTGT TCTAAGTGCT
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19851 AGAGGGAAAC CCTGGGGAAA CAACGGGCTT TCCTGCTTCG TGAAATTTGT
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19951 CCCTAATCAT GTTCAGCTAC TCTAGTTGGT ATGTATACTT GATTAGTCAT
20001 AGCACTTATA AATAATTTAT ATTTTATATA ATATATACTT ACATATTATA
20051 GACCATTCAC AGATACAAAT CACACACATA AACACACACC TTTTCAACAG
20101 CATTGTGAGG GACAAAGCAG GCAAAGTGAG GCTGGTTATC AGACTTTAAC
20151 AGATTAGAAA ATATATTCCC AGGAGGACAG GAATTCCCCA AGGTCAGGCA
20201 GCTAGCCAAT AGTTTTTCTA AGCTGAGTAA AACCTTCCCT GCCTCTAACG
20251 GCCCACAAAG GAGGGAAGAC CGCGATACAC ACCTGTCTGG TATAAGGGGG
20301 AAGACCACAG CCGTGCTGTT TTTGTGAGGC AGGTAAGGGA AGGGGCAAGA
20351 GGATAAGTCA TGTGTCAGGA AGCAGCGTCC AACCAGAGCC GGCCACCTGT
20401 CCCTTTTCCT GCCACCATGC ACCAACTTTG CTGTTCAGTC ACTGAAGCTC
20451 ATTCTGCACT GGCTTCCTCC CTTCCAGGCT CCAGGGGATG CTGAGCTCTC
20501 CTTGTACGAC TCAGAGGAGG ACATTCGCAG CTACTGGGAC TTAGAGCAGG
20551 TGAGCTGAGG GAAGGGGCTG TGAGGGTGGG AGCAGGGCGA AGAGGGGAAG
20601 GATGGGGTCG CTGTCAAATA CAAGGCGTTC ACTCAGCTGT CTCACCTCCA
20651 GCCCAGAGCA GTCACATTCA AGGCCACAAA GATTGTGGT CATCTTTGTT
20701 TTTTTTCTTT TCCTTTTCTT TTTTTTTTTT TTTTAATTTG AGACAAAGTC
20751 TCACTCTATC ACCCAGACTG GAATGCAGTG GCATGATCTC AGCTCACTGC
20801 AACCTCTGCC TCCCGGGTTC CAGAGGTTCT CCTGCCTCAG CCTCCCCGAGT
20851 AGCTGGGACT TCAGGCCTGC GCCCAGCTAA TTTTTGTATT TTTAGTAGAG
20901 ACAGCTTTTC ACCATGTTGG CTGGGCTGGT CTCGAACTTC CGATCTCAAG
20951 CAATCTGCCT GCCTCGGTCT CCTAAGTGCC TGGATTACAG GCATAAGCCA
21001 CGATGCCTGG CCTTTGTTTT CATTCTTCTC ACTCCCTGAA AGGCATCGTG
21051 GGGAGAGGGT GAGTCACTGG ACCAAGTCCT AGAGAACCAG TATCTATTCT
21101 TATTCTCCAA CACATCACCC ACGTGACCCT GAGCAAGCCA CATACACCCT
21151 GGGCCCTAGT TTTTATCATC TGTGAAATTA GGGGAAACAT AGGTAATACC
21201 TGTCCCATCC ACCACACAAG ATTGGCAGGG CAGTCACTTG TTCTTTCATT
21251 AATTCAGCAG GTATTTATGG CGTACCTACT GTTTGCCTGA CACAGTTCAG
21301 GATGGGCACA TAGCAGTGAG CAAAACAAAG GCCTCTGCCT TTTAGAAACT
21351 TACGTTATGG TAGAATAGAT GGATTTNNNN NNNNNNNNNN NNNNNNNNNN
21401 NNNNNNNNNN NNNNNNNNNN NNNNNGTCT ACAAATGAAT TATTATTGCA
21451 TGTGGACAAG CCTTAAGAAC TAAAAAATAT GTGGCTGGGT GCAATGGTTC
21501 ACACCTGTAA TCCCAGCACT TTGGGAGGCT GAGGTGGGCG GACCACCTGA
21551 GGTCAGGAGT TTGAGACCAG CCTGGCCAAC ATGGCGAAAC CCCGTCTCTA
21601 CTAAAAGCAC AAAAATTAGC CAGGCGTAGT GGTGCATGCC TGTAGTCCCA
21651 GCTACTCGGA AGTCTGAGGC ATGAGAATCA CTTGAACCTG GGAGGCAGAT
21701 GTTGCAGTGA GCCGAGATCG TGCCACTGCA CTCCAGCTTG GGTGACAGAG
21751 CTAGACTGTC TCAAAAACAA ACAAACAAAA CAAAACCTAA AAGATATGTG
21801 GATATGAGGG ATCACCATCC CCATAGGGCC CCTGGATTAA CACCACCCCA
21851 CCAATGCCCT GAATTAAAAG AAACCAGATG ACTAGGTTTG GAGAAATCTG
21901 GCTTTGGGTC TATGAGAAGT AGTGTCTCTC TTTGTGCCTC TTCCCATTCT
21951 TTTTGACATT GAGCTCCATG GTGCTCTGAA TCCGTCTCTC ACAGTGCTGA
22001 TGGCAGGTGG GACAGATTAG AAAATAGAGC TGGAGCCACA GAGATTTGGC
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22051 AGACTGATTT CGGTGCCCTC TTGGAATCTC CAGCACATTC CAAAAAGCCT
22101 GGATAGGACC AAAATAGCTT ATCAACGTGA GAAAGGACTT CAGAGCTTGT
22151 CTACTGCCAA CCCTCATTTT ACCCAATGAG GAAAGTGAAG CTATTAGGGG
22201 GCGAGGGACA CGTGGAAGGT CACACAGCAC ACAGGAGGTG ATTCACATGT
22251 AGATTTCAGC ACCTGCTCCT GCCACGCTGG ACTGGTTCAC CTCCTAGGCT
22301 GACCCTGCCT CTCCCCTGTT CACACACACT CTCGCACACA CACACACACA
22351 CACACACACA CACAGGTGCT TTGTTCTGGC CAGGGGTTCC TAGGGTCACC
22401 TCTTGGTTGC AGCCACTGTG ACCCCAACTG GTCTAACCTC TCTCTTCCCC
22451 TCCCACTTCC TTCCTGTGGT TCCTGCAGGA GATGTTCGGG AGCATGTTTC
22501 ACGCAGAGAC CCTGACCGCC CTGTGAGGGC TCAGCCAGTC CTCATGCTGC
22551 CTACAGAGTG CCTGGCACTT GGGACTTCCA TAAAGGATGA GCCTGGGGTC
22601 ACAGGGGGTG TCGGGCGGAG GAAAGTGCAT CCCCCAGAGC TTGGGTTCCT
22651 CTCTCCTCTC CCCCTCTCTC CTCCCTTCCT TCCCTCCCCG CATCTCCAGA
22701 GAGAGCCTCT CAGCAGCAGG GGGGTGCTAC CCTTACAGGA GTGAGAGTCT
22751 GGTGAGCCCA CTCTTCACCC GTCAGGCCCT GGCCGCAATG GACAAGCCTC
22801 CTGCTCACTC CACCCCACCC ACCTCTGCCC TGTCCTTGGC AGCTGAAGGA
22851 CACCTTGACT TCCAGCTTTT ACGAGTGAGC CAAAAACAGA AGGACAAGTA
22901 CAACTGTGCT GGCCTGCTGT ACAAGCTTCA AAAAGTGTCC CAGAGCCCAC
22951 ACGGCTCGGT GTCAGATGGT GTCAGGCTGT CACGGACATA GGGATAAACT
23001 TGGTTAGGAC TCTGGCTTGC CTTCCCCAGC TGCCTCAACT CTGTCTCTGG
23051 CAGCTCTGCA CCCAGGGACC ATGTGCTCTC CACACCCAGG AGTCTAGGCC
23101 TTGGTAACTA TGCGCCCCCC GTCCATCATC CCCAAGGCTG CCCAAACCAC
23151 CACTGCTGTC AGCAAGCACA TCAGACTCTA GCCTGGACAG TGGCCAGGAC
23201 CGTCGAGACC ACCAGAGCTA CCTCCCCGGG GACAGCCCAC TAAGGTTCTG
23251 CCTCAGCCTC CTGAAACATC ACTGCCCTCA GAGGCTGCTC CCTTCCCCTG
23301 GAGGCTGGCT AGAAACCCCA AAGAGGGGGA TGGGTAGCTG GCAGAATCAT
23351 CTGGCATCCT AGTAATAGAT ACCAGTTATT CTGCACAAAA CTTTTGGGAA
23401 TTCCTCTTTG CACCCAGAGA CTCAGAGGGG AAGAGGGTGC TAGTACCAAC
23451 ACAGGGAAAA CGGATGGGAC CTGGGCCCAG ACAGTCCCCC TTGACCCCAG
23501 GGCCCATCAG GGAAATGCCT CCCTTTGGTA AATCTGCCTT ATCCTTCTTT
23551 ACCTGGCAAA GAGCCAATCA TGTTAACTCT TCCTTATCAG CCTGTGGCCC
23601 AGAGACACAA TGGGGTCCTT CTGTAGGCAA AGGTGGAAGT CCTCCAGGGA
23651 TCCGCTACAT CCCCTAACTG CATGCAGATG TGGAAAGGGG CTGATCCAGA
23701 TTGGGTCTTC CTGCACAGGA AGACTCTTTA ACACCCTTAG GACCTCAGGC
23751 CATCTTCTCC TATGAAGATG AAAAATAGGGG TTAAGTTTTC CATATGTACA
23801 AGGAGGTATT GAGAGGAACC CTACTGTTGA CTTGAAAATA AATAGGTTCC
23851 ATGTGTAAGT GTTTTGTAAA ATTTCAGTGG AAATGCACAG AAAATCTTCT
23901 GGCCTCTCAT CACTGCTTTT CTCAAGCTTC TTCAGCTTAA CAACCCCTTC
23951 CCTAACAGGT TGGGCTGGCC CAGCCTAGGA AAACATCCCC ATTTCTAACT
24001 TCAGCCAGAC CTGCGTTGTG TGTCTGTGTG TTGAGTGAGC TGGTCAGCTA
24051 ACAAGTCTTC TTAGAGTTAA AGGAGGGGGT GCTGGCCAAG AGCCAACACA
24101 TTCTTGGCCC AGGAGCATTG CTTTTCTGTG AATTCATTAT GCCATCTGGC
24151 TGCCAATGGA ACTCAAAACT TGGAAGGCGA AGGACAATGT TATCTGGGAT
24201 TCACCGTGCA CAGCACCCGA AGTGCCAAAT TCCAGGAGGA CAAGAGCCTT
24251 AGCCAATGAC AACTCACTCT CCCCTACTCC ACCTCCTTCC AAGTCCAGCT
24301 CAGGCCCAGG AGGTGGGAGA AGGTCACAGA GCCTCAGGAA TTTCCAAGTC
24351 AGAGTCCCCT TTGAACCAAG TATCTAGATC CCCTGAGGAC TTGATGAAGT
24401 GATCCTTAAC CCCCAAGTAA TCATTAACCC CCAGACCAGC CTCAGAACTG
24451 AAGGAGATTG TTGACCCAGT GACCTGGAGT TGAGGCTCAG GGAGAGATCT
24501 GCCACATGTC TGAGGGTTGC AGAGCC
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FEATURES:

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Start:    1997
Exon:     1997-2121
Intron:   2122-4732
Exon:     4733-4872
Intron:   4873-5004
Exon:     5005-5115
Intron:   5116-5781
Exon:     5782-5957
Intron:   5958-7770
Exon:     7771-7935
Intron:   7936-8470
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Exon:      8471-8623
Intron:    8624-8917
Exon:      8918-9000
Intron:    9001-9777
Exon:      9778-9925
Intron:    9926-10221
Exon:      10222-10335
Intron:    10336-10539
Exon:      10540-10617
Intron:    10618-11197
Exon:      11198-11293
Intron:    11294-13338
Exon:      13339-13445
Intron:    13446-14214
Exon:      14215-14284
Intron:    14285-14400
Exon:      14401-14493
Intron:    14494-15980
Exon:      15981-16262
Intron:    16263-17597
Exon:      17598-17652
Intron:    17653-18842
Exon:      18843-18988
Intron:    18989-20477
Exon:      20478-20549
Intron:    20550-22478
Exon:      22479-22523
Stop:      22524
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CHROMOSOME MAP POSITION:
Chromosome 1

ALLELIC VARIANTS (SNPs):

DNA Position	Major	Minor	Domain	Protein Position	Major	Minor
48	C	G	Beyond ORF(5')			
132	G	A	Beyond ORF(5')			
724	A	C	Beyond ORF(5')			
1558	C	G	Beyond ORF(5')			
1577	A	G	Beyond ORF(5')			
2487	C	A	Intron			
2634	T	C	Intron			
4352	A	G	Intron			
5157	A	C	Intron			
5658	A	T	Intron			
5945	T	C	Exon	180	T	T
6281	C	T	Intron			
6452	G	C	Intron			
6610	T	G	Intron			
7247	T	C	Intron			
7360	A	G	Intron			
7644	A	T	Intron			
8127	A	C	Intron			
8317	G	A	Intron			
9079	G	A	Intron			
9537	G	T	Intron			
12302	C	G	Intron			
12354	C	T	Intron			
12487	C	T	Intron			
13198	–	A	Intron			
13257	A	G	Intron			
14541	G	A	Intron			

14545	A	G		Intron			
15041	C	A		Intron			
15053	A	C		Intron			
15065	A	G		Intron			
15108	A	C		Intron			
16274	–	G		Intron			
17424	C	T		Intron			
17627	G	A		Exon	657	V	V
18427	T	C		Intron			
18813	C	G		Intron			
19035	T	C		Intron			
19182	T	C		Intron			
19508	–	G	C	Intron			
19571	T	G	C	Intron			
20147	T	G		Intron			
20180	G	A		Intron			
20584	A	T		Intron			
20717	T	C		Intron			
20894	A	G		Intron			
21787	–	A	C	Intron			
22264	T	C		Intron			
22338	–	C	A	Intron			
23363	T	C		Beyond ORF(3')			
23688	G	A		Beyond ORF(3')			
24210	A	C		Beyond ORF(3')			

Context:

DNA
Position
48   CTGGGTTCCTATGTGGGGAGGTCATGCTCCCCACTCATTGAGCCCCC
[C,G]
CAGGCAAACCACCTGGACAGCCAGACCCATGCAGACTCTGGAGCAGGTGGAGAGGAAGAG
TGAGACCACCCCGCCTCACGGGCGGTGAAGGGCCGGCAGCCTCTGAATAGTCTCTGCTAG
GAGGTAGAAAGCACCCTCCCATCTTAATCATAGTAATCATCGCCACTACCATTTACTGGG
TGCCTATAAAAGGCCAGCCTCTTCATACACATGATCTCACTGAATCCTCATAGCATCTGC
CTGCGACTGTTATTATCCCCATTTACAGATGAAGAAACTGAATCTTTGAACCCAGGTCAT

132   CTGGGTTCCTATGTGGGGAGGTCATGCTCCCCACTCATTGAGCCCCCCCAGGCAAACCAC
CTGGACAGCCAGACCCATGCAGACTCTGGAGCAGGTGGAGAGGAAGAGTGAGACCACCCC
GCCTCACGGGC
[G,A]
GTGAAGGGCCGGCAGCCTCTGAATAGTCTCTGCTAGGAGGTAGAAAGCACCCTCCCATCT
TAATCATAGTAATCATCGCCACTACCATTTACTGGGTGCCTATAAAAGGCCAGCCTCTTC
ATACACATGATCTCACTGAATCCTCATAGCATCTGCCTGCGACTGTTATTATCCCCATTT
ACAGATGAAGAAACTGAATCTTTGAACCCAGGTCATCTGGCTCTCAAACTTGTGCTGTTT
TCCCTAAGCCACCCGGTCTCTCATTTCTCCCACTGAAATGTCTCACATGCCATTGCCCTT

724   ATTGCCCTTACTCATTTCTGCCCATGTCTCCTCCAAAACACCATTTATCAATTCGCTCAA
CAAGTATGTGTTGAGTACACACTAAGGGCCAGGCGAGGGGCTGGGCACAGGCGCTGGGGG
TAGGTTCATTCTCCCACCTTCGCTTCTGCTGGGTATCACCTGTGGGGTCTTGCCGGGCAT
CCCACCCTCACCTGTAGTTCAAGTGGACCTTGGGATCCCAAGACCAAATGAATGGAATGC
ACCAGCCCAGCCTTCACCAACTTGAGCACAATCTTATTCATAATAGAAACTCACATTTGC
[A,C]
TCACACTTTACATTTTACACAACCCCTTCTTATCCATTAACTCATTTGATCTTCACAACA
ACCCTGTGAGATATGTCTGTTACTCCCACTTTAGTGATACAGAATCTGAGGTTTGAAAAG
TAATGCTGACCATTCTGCCTCATTAATAAAAGCAGGATTAACCCAGGCTCCTGGACCCTT
CCACAAAAGGCATTAAGCAACCTGCTCCCCTCTGACAACCTCCCCTGTCACCCAGGCTCT
CCTCTGGGAAGTTGGGGGCATCTCTAGCCCCCAAGTAGTTACTCATTTTCAACCCCATCT

1558 TCAGCTCTGCCCATCTCAGCTCCTGGAACGTCAGCCAGGTTGCGCAAAAAGTGAGGAGGA
GAGGAGCGGCAGTACACAAGGGTGGGGGAAAGATTAGGCACAGGAAGCCGTGGGAGAGAG
AGCCGGCAGGTGGACCATCCTGGTTTCCCCACACACACCATTGTCCCCCTGGGAAACCTG

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        TTGGTGAAGTTCTAGATGTCTTATCCAAGAAGGGTCCTCTTGAGGTCATCTCAGCTATCC
        CCCTGCCTCTAGGCAAGCTGTTTTCTGTTTCTTCCAAGCTGACTGGCTGAATGGTAGGAG
        [C,G]
        CTTTCTGCCAGGGAAACTAAGGTCTGGGAAGGGAGTATGGCTTGTGGGGACACCAGGGGT
        CAGGGGAGGGGAGGGTCCACCTGCTGAATCAAGTGGGGCCTCCTGCCCTCGTGATTCCCC
        TTTGCCTGGTGCTCAGTGGGGGTGATGGTGACGCCACAGGTGTGGAGTGCCAGCCACGTG
        CTGAGCGCCAAGCAAAACAGCCAGGGTGAGTCTATGCATCATCAGTGCCTGGGAAGGAAG
        GCCACTGCGAGCAGGGAGTCTGACGGAAAAACTTGACAGAGGGAAGGGAGGCACCTTGCT

1577    CTCCTGGAACGTCAGCCAGGTTGCGCAAAAAGTGAGGAGGAGAGGAGCGGCAGTACACAA
        GGGTGGGGGAAAGATTAGGCACAGGAAGCCGTGGGAGAGAGAGCCGGCAGGTGGACCATC
        CTGGTTTCCCCACACACACCATTGTCCCCCTGGGAAACCTGTTGGTGAAGTTCTAGATGT
        CTTATCCAAGAAGGGTCCTCTTGAGGTCATCTCAGCTATCCCCCTGCCTCTAGGCAAGCT
        GTTTTCTGTTTCTTCCAAGCTGACTGGCTGAATGGTAGGAGCCTTTCTGCCAGGGAAACT
        [A,G]
        AGGTCTGGGAAGGGAGTATGGCTTGTGGGGACACCAGGGGTCAGGGGAGGGGAGGGTCCA
        CCTGCTGAATCAAGTGGGGCCTCCTGCCCTCGTGATTCCCCTTTGCCTGGTGCTCAGTGG
        GGGTGATGGTGACGCCACAGGTGTGGAGTGCCAGCCACGTGCTGAGCGCCAAGCAAAACA
        GCCAGGGTGAGTCTATGCATCATCAGTGCCTGGGAAGGAAGGCCACTGCGAGCAGGGAGT
        CTGACGGAAAAACTTGACAGAGGGAAGGGAGGCACCTTGCTTTATCGGGGCGGGGAAGGC

2487    ACACGGCTTCTGCACTGGTATCCCTAAGATGGGGTTAAGGGAAGCCCTGGGGAAGTGAGG
        TTCTGAATGATGAATTTAAGATCCTACAACCTCATCTGTACTGAGACCCCCAGGGAGGAT
        GGGGAGCAGGAGCAAGAACCATCCAGAAGGGTTATATGGCATTCCCAAACCCCTGCATGG
        CATCTCCCATATTCTCAATTCACCCGGGTCTCTCTGGGTTTGTTAAGGCATGGTAGATGA
        GCATCTACGTTATGGAGGGGTGGGGAGCATCAGAGCCCTTACTCCATGCCCTGTTCCCTC
        [C,A]
        TTACAAAAAATACCTGAAGTTACCATCACCCCAGGTTCTTTGTCCTTTCCCTCCCGGATG
        TTCCTTCCTCCACTTGGTCCAGAGAATGCCAAAAGGAGGCCCTAAATTTCTGAACTTTCC
        TGAGGGGACCTACCAGGGTGTAGTCCTACCAGCGCCCAGGGTCTTTCCACTCTCATCTCC
        CTGGAAATGCGATGGTGGGTATGAAACCTTGTCCCTAAGTAGGCGCTACACAAGGTGATC
        CATACCCACACCCCAGGAGGCTGGGGCTGCGGGTGTCACCCTCCCCATTCCCAGACTCCT

2634    AGGGTTATATGGCATTCCCAAACCCCTGCATGGCATCTCCCATATTCTCAATTCACCCGG
        GTCTCTCTGGGTTTGTTAAGGCATGGTAGATGAGCATCTACGTTATGGAGGGGTGGGGAG
        CATCAGAGCCCTTACTCCATGCCCTGTTCCCTCCTTACAAAAAATACCTGAAGTTACCAT
        CACCCCAGGTTCTTTGTCCTTTCCCTCCCGGATGTTCCTTCCTCCACTTGGTCCAGAGAA
        TGCCAAAAGGAGGCCCTAAATTTCTGAACTTTCCTGAGGGGACCTACCAGGGTGTAGTCC
        [T,C]
        ACCAGCGCCCAGGGTCTTTCCACTCTCATCTCCCTGGAAATGCGATGGTGGGTATGAAAC
        CTTGTCCCTAAGTAGGCGCTACACAAGGTGATCCATACCCACACCCCAGGAGGCTGGGGC
        TGCGGGTGTCACCCTCCCCATTCCCAGACTCCTGGCAGACCTCCTCTGGCCCAGCTATAG
        GCCAACTCACTCTCCCTCACTCCCTTGGGGAAACGGCTGATTCAGTTACCTGGATTGAGG
        TCACTGGCAATGGCTGAAGTGGAGACGCAGGTGGAACTGGTTCAGGCCGGGGGAATCACC

4352    ATTGGAGTTACCACACATAAAGGATAGTGAGTCAGCAGAGTGCACCCTGCAGGAACAATA
        GAGCCTTCCTTTTCAAGGAAGTTCTAAGAAAAATGGCAGCAGGCAGGCCCCACTCGGGTG
        TATTCACTCATTCATTTATTCAACAAATATTTACTAAGTGCCCCTGTGCAAGGCTCGAGG
        TGTACAAAGATGAACAGGAGAGCTAGACTTCTTGCCATGCGTGGTGGGGTTTGCTGCCTA
        GTGGGAGAGACAGACAAAAAGCAAGGAATGCACACACAGGATGCACACACAGCGGCAGGA
        [A,G]
        CCAAGGTGCAGTTACCCAGGCCTGGGATCAGACAGACAGGACTCAGAGGAGACTTTCCCA
        GAGAAAAGCCATCTGAGCCAAGGGATGGATCTGATACCTCCGAAGGCTGAGCCACCATAA
        CACTCATACCTTTAAGCCAAGTCTTATAAACTCCCCAGGTAAGCAGCTGGCAGTCAGAAG
        ACCTCCAGCTAATGCCCAGGACAAGTTGATGAGCTCTCAAGAAAAAGTTCCTGCCTTTTC
        TTCTCAATATCCCTGGCACACAGTTCAGTGAATTTTGAATGAACCAATGAATGAAATGAG

5157    ATCCAGGTCCCACAAGGTGAAGGGGCTCCTTCAGCCAGGCCTGGATTGCCACTCCCCTCA
        CCATTCCTCTCCTCATCCCCACTCCATCCCTCTGTGATCCCCATAAGCTAGTCATGCTGC
        TGAGCTTCAGTCTCGTTGTCCTCTGCAGGCATGGCATTTGCTCTGCTGGCCAACCTTCCT
        GCAGTCAATGGCCTCTACTCCTCCTTCTTCCCCCTCCTGACCTACTTCTTCCTGGGGGGT
        GTTCACCAGATGGTGCCAGGTAAGGCCTCTCCCCTCTGGGCAGGCAGGATGACCCAGACC
        [A,C]
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FIGURE 3, page 11 of 20

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        CAAGGATGGGAGGTGTGGCAAAGGGGCCTCGGGAGATTTTCCATCTGCATTCTCCTGGAG
        TTGTTCCTGGTCAGTCCTAGGGGAATGGTCACTGTGAATGTCATTTCCAGGTCCTCGGTG
        ACCTTGGAGAAACCACTGAGCCTCTTTGAGTTCAGTTAGCATTACCTGTTCCATCTTCCT
        CCTAGGAATGAGAGGAAGACTTAGCAGAACAAGATATACCATATGCTATAACATGCTTAA
        ACAGATGTGAGAAATCACCATCTAACTCCCTGGTTGGTCCCAGCCGGCCACTACAGGGAC

5658    TTAGCAGAACAAGATATACCATATGCTATAACATGCTTAAACAGATGTGAGAAATCACCA
        TCTAACTCCCTGGTTGGTCCCAGCCGGCCACTACAGGGACATTTGGACTTCTCTGGTGCT
        AAGTGAGATGGAGGAAAGCCTGGTCACAAGGGCTGGTTTCTGGTTCAGGCTCTGCTTATA
        TTTCTTATTTCTGAGTTCATTTTCTCACGTGTCCTGTATGACAATATTGACCATTGGGGT
        AAAAGCACCTTGAAAAGCATAGATCATGGTTAGAGTGAGTGGTTGTTATTATTGTGTTGG
        [A,T]
        GAAGAGCCTTGGAGGTGCAGGGATCCATCCCCCTGGGGTCGGGAAGCATTCCTGGGCCCC
        TTTCTGGTTTCCATCGGTGTGGTTCAAACCTCTGATTTTTGCTGGCTGGGTGGGGCACCA
        CAGGTACCTTTGCCGTTATCAGCATCCTGGTGGGTAACATCTGTCTGCAGCTGGCCCCAG
        AGTCGAAATTCCAGGTCTTCAACAATGCCACCAATGAGAGCTATGTGGACACAGCAGCCA
        TGGAGGCTGAGAGGCTGCACGTGTCAGCTACGCTAGCCTGCCTCACTGCCATCATCCAGG

5945    ATTATTGTGTTGGAGAAGAGCCTTGGAGGTGCAGGGATCCATCCCCCTGGGGTCGGGAAG
        CATTCCTGGGCCCCTTTCTGGTTTCCATCGGTGTGGTTCAAACCTCTGATTTTTGCTGGC
        TGGGTGGGGCACCACAGGTACCTTTGCCGTTATCAGCATCCTGGTGGGTAACATCTGTCT
        GCAGCTGGCCCCAGAGTCGAAATTCCAGGTCTTCAACAATGCCACCAATGAGAGCTATGT
        GGACACAGCAGCCATGGAGGCTGAGAGGCTGCACGTGTCAGCTACGCTAGCCTGCCTCAC
        [T,C]
        GCCATCATCCAGGTGAGGGGGCAGCCCCCAACCCTGCTAGAAGGGCATCAGACCACCCTG
        CCCCTCCCTCAAAGCCTTAGCTTTGATGCTAAATCTGATTTAGGGGGCTGGGTGTGGAGG
        CTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGAGGGTGGATCACTTGAGGTCAGG
        AGTTTGAGACCACCTTGACCAACGTGATGAAACCCCATCTCTACCAAAAATACAAAAATA
        ATCCAGGCTTGGTAGTATGCGCCTGTAGTCCCACCTACTCAGGAGGCTGAGGCAGGAGAA

6281    GCTAGAAGGGCATCAGACCACCCTGCCCCTCCCTCAAAGCCTTAGCTTTGATGCTAAATC
        TGATTTAGGGGGCTGGGTGTGGAGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGA
        GGAGGGTGGATCACTTGAGGTCAGGAGTTTGAGACCACCTTGACCAACGTGATGAAACCC
        CATCTCTACCAAAAATACAAAAATAATCCAGGCTTGGTAGTATGCGCCTGTAGTCCCACC
        TACTCAGGAGGCTGAGGCAGGAGAATCACTTGAATCCGGGAGGCAGAGGTTGCAGTGAGC
        [C,T]
        GAGATCGCGCCACTGCACTCCAGCCTGGGTGACAGAGCGAGACTCCGTCTCAAAAAAAAA
        AAAAAAAAAAAAAAAAAAACCCAAGTTAGGGCTCACCTCCTCCCTCCTCCCCATCCCAGG
        GCTAAAGTGAACCTTGAAAATTAACAGTATCTCCTCATCTGCATGTAGCAGGACCATACA
        AAAAAACAACAGCTGTACCTGGTTAAACTGTCCTGAGCTTTAAACCTGTAAAAGACTCAC
        AGCCTCTCTCCATTATCCCGTGGAGAAACCCAACTCTCTGCCAGCATAGTCTTGCAGACT

6452    ATGAAACCCCATCTCTACCAAAAATACAAAAATAATCCAGGCTTGGTAGTATGCGCCTGT
        AGTCCCACCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAATCCGGGAGGCAGAGGTT
        GCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGGTGACAGAGCGAGACTCCGTCT
        CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACCCAAGTTAGGGCTCACCTCCTCCCTCCTCC
        CCATCCCAGGGCTAAAGTGAACCTTGAAAATTAACAGTATCTCCTCATCTGCATGTAGCA
        [G,C]
        GACCATACAAAAAAACAACAGCTGTACCTGGTTAAACTGTCCTGAGCTTTAAACCTGTAA
        AAGACTCACAGCCTCTCTCCATTATCCCGTGGAGAAACCCAACTCTCTGCCAGCATAGTC
        TTGCAGACTGCTAATTTTCTCTAACATCCCTCACTCCGCTCCAGCCTCCTCTGCTCCAAG
        CCACAGCAGCAGTTGCACAACATAAATTGAGCTTCTGCAAATGGTTGCAAAGGATTCTGC
        TAGGTTTTATGAAGGGAAGCACAACATGACAGAATGCAAGAGCAAAACACAGTCCCAGAG

6610    GTGACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACCCAAGTTA
        GGGCTCACCTCCTCCCTCCTCCCCATCCCAGGGCTAAAGTGAACCTTGAAAATTAACAGT
        ATCTCCTCATCTGCATGTAGCAGGACCATACAAAAAAACAACAGCTGTACCTGGTTAAAC
        TGTCCTGAGCTTTAAACCTGTAAAAGACTCACAGCCTCTCTCCATTATCCCGTGGAGAAA
        CCCAACTCTCTGCCAGCATAGTCTTGCAGACTGCTAATTTTCTCTAACATCCCTCACTCC
        [T,G]
        CTCCAGCCTCCTCTGCTCCAAGCCACAGCAGCAGTTGCACAACATAAATTGAGCTTCTGC
        AAATGGTTGCAAAGGATTCTGCTAGGTTTTATGAAGGGAAGCACAACATGACAGAATGCA
        AGAGCAAAACACAGTCCCAGAGAGCGCCTTTTCATTCACTCATTCATTCGGTTTTGTGCC
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FIGURE 3, page 12 of 20

AAGAACTAGGCTAAACCCTGGGATACAAAGATAAGTAAGAAAGAGGTCCAATTCACAAGT
TGCTCACAGCCCAGCAGAGGAAGGAGCCATGTCAACAGATAAATTTGTATGCAGTGAGAT

7247   GACACAGAGCAGAGTCACGGAGGACCTCAAAGAGGAGGTGACACTCCACCTCTCTTAAAG
GATGAGAACTTAACCAGGAACAAGGTATACAGAGGATGGTCCAGGCAGAAGGGAACAGTG
CCTAAAAACACTGAGGCCTGAGAGAGTGTGATCTGCGCAGGCAAAGTAAGGGGCTTGGTG
TGGCTGGAGGGTAGAGGGCCCAGAAGAGGATGGAAAAGTAGGCAGGAGCCAGACAATGAG
ATCTGGGGTCTGTTCTCTGACAGCGACTTTGGGTCTGATTGGCAGTTTATAAGGATCGTT
[T,C]
GGGCTACACAATGATGAGTGGGAGGTGGATTAGAATCAAGGCAGGGGACCTGTTGGGAGA
CTCTGCAGAGGCCCAGGCAGGAATAATGCAGGCGAAGACCAGGTAGAGAAAGAGATGGGG
CTGGACTTGAAAAGAATGTTTTACCAGGAGCTTGGTGATAGACTGGATGTGGGAGGTAAG
GGAGGATGACTCTCAAGTTTTTGGTTGGGCAACCAGGTTAATGATGGTGTCATTTACTGA
GAGAGAAAACACTGGGGGAGGACTAGACTTATTTTACAGATAAGCCAAAGCCAGAGAGGT

7360   AACAGTGCCTAAAAACACTGAGGCCTGAGAGAGTGTGATCTGCGCAGGCAAAGTAAGGGG
CTTGGTGTGGCTGGAGGGTAGAGGGCCCAGAAGAGGATGGAAAAGTAGGCAGGAGCCAGA
CAATGAGATCTGGGGTCTGTTCTCTGACAGCGACTTTGGGTCTGATTGGCAGTTTATAAG
GATCGTTTGGGCTACACAATGATGAGTGGGAGGTGGATTAGAATCAAGGCAGGGGACCTG
TTGGGAGACTCTGCAGAGGCCCAGGCAGGAATAATGCAGGCGAAGACCAGGTAGAGAAAG
[A,G]
GATGGGGCTGGACTTGAAAAGAATGTTTTACCAGGAGCTTGGTGATAGACTGGATGTGGG
AGGTAAGGGAGGATGACTCTCAAGTTTTTGGTTGGGCAACCAGGTTAATGATGGTGTCAT
TTACTGAGAGAGAAAACACTGGGGGAGGACTAGACTTATTTTACAGATAAGCCAAAGCCA
GAGAGGTGATGTGACAGAAAGGCCCATGCTCTAAAGGAGCTGAAGGTCTGATGGCAGCCA
TGTAGAGCACAGTGAAGGGCAGGTGAAGGTCACAGATGGTCCAATTCCCTCAAGCTACTG

7644   GACCAGGTAGAGAAAGAGATGGGGCTGGACTTGAAAAGAATGTTTTACCAGGAGCTTGGT
GATAGACTGGATGTGGGAGGTAAGGGAGGATGACTCTCAAGTTTTTGGTTGGGCAACCAG
GTTAATGATGGTGTCATTTACTGAGAGAGAAAACACTGGGGGAGGACTAGACTTATTTTA
CAGATAAGCCAAAGCCAGAGAGGTGATGTGACAGAAAGGCCCATGCTCTAAAGGAGCTGA
AGGTCTGATGGCAGCCATGTAGAGCACAGTGAAGGGCAGGTGAAGGTCACAGATGGTCCA
[A,T]
TTCCCTCAAGCTACTGCTACGCTAGGACTGCACGGAGCTCCAGACCTGCGTGTGTGTGGG
GCGGGTCGTTGGAACTGCTGAACCACATTGGTCTTCCGCCACCAACCACCCTTTTCCTCC
TCTCAGATGGGTCTGGGCTTCATGCAGTTTGGCTTTGTGGCCATCTACCTCTCCGAGTCC
TTCATCCGGGGCTTCATGACGGCCGCCGGCCTGCAGATCCTGATTTCGGTGCTCAAGTAC
ATCTTCGGACTGACCATCCCCTCCTACACAGGCCCAGGGTCCATCGTCTTTGTGAGTCTG

8127   CATCCGGGGCTTCATGACGGCCGCCGGCCTGCAGATCCTGATTTCGGTGCTCAAGTACAT
CTTCGGACTGACCATCCCCTCCTACACAGGCCCAGGGTCCATCGTCTTTGTGAGTCTGGG
GATGCACCCCTGCCATTGGAGCAAGGCTCCAGCAGACACATGAGGAGGATGTACTGTTTT
AAGATGTCGTGAGCTCCTCATTGCAAGGGCTGGCTTAGCTGTTGTTCAGAGAGGATTCTG
AGGGGGTTTCTGTCTTGGGAGGGTCAAAGTCATGACTCACAGAGGTTCTTGGTAGTTAAT
[A,C]
CCTGCAGAAAAGAGCTGTACATTCTCCGCCAGTTCCCCATTCTAGTGCCTCAACCCCTCC
CTGCCTGGAAAGTCCTGCCTTATGTCTAATCTCCATCCCTCCTCCTTCAGCCCAAACTCT
TCTAAAGAAAAAGAAAGCATTCCTTTTCTAGCACAAGTTCCCCATGTGCCTTTTGGGAAA
GGGCGGTGGGCGACGGGACAGGGTTCCTGATCAGGGTTTTAATTCTGTCTTGGTGTGCCT
CCATTAGCTTTGATGGCATCCCTTCCCTGGGTCAGACACCCAAAGGTGGGGTATTATGGG

8317   GAGCTCCTCATTGCAAGGGCTGGCTTAGCTGTTGTTCAGAGAGGATTCTGAGGGGGTTTC
TGTCTTGGGAGGGTCAAAGTCATGACTCACAGAGGTTCTTGGTAGTTAATACCTGCAGAA
AAGAGCTGTACATTCTCCGCCAGTTCCCCATTCTAGTGCCTCAACCCCTCCCTGCCTGGA
AAGTCCTGCCTTATGTCTAATCTCCATCCCTCCTCCTTCAGCCCAAACTCTTCTAAAGAA
AAAGAAAGCATTCCTTTTCTAGCACAAGTTCCCCATGTGCCTTTTGGGAAAGGGCGGTGG
[G,A]
CGACGGGACAGGGTTCCTGATCAGGGTTTTAATTCTGTCTTGGTGTGCCTCCATTAGCTT
TGATGGCATCCCTTCCCTGGGTCAGACACCCAAAGGTGGGGTATTATGGGAAGAAGGGGT
GGGAGCCTGTGAGCATGATGCTCTTTCCCCCAGACCTTCATTGACATTTGCAAAAACCTC
CCCCACACCAACATCGCCTCGCTCATCTTCGCTCTCATCAGCGGTGCCTTCCTGGTGCTG
GTGAAGGAGCTCAATGCTCGCTACATGCACAAGATTCGCTTCCCCATCCCTACAGAGATG

9079   TTCTACTGCTCTAATAATTCCCCCTAAGGAGGCAGGGGAGTGGGATTCAGGGTCCCCAGA
GAAAAGGGAGACTTGAGAGAGACGCCTGCCCTGGCCCCACCTTAGGGCCAATCCCCATTC
TCCACTCTGGGGTTTGCAGGTGGTGGTGGCAACAGCTATCTCCGGGGGCTGTAAGATGCC
CAAAAAGTATCACATGCAGATCGTGGGAGAAATCCAACGCGGGTGAGTCCAGGTGGCCCA
GAAGCCTGGCCCACCCGCACCTCATGCCCCACTAAGGCCTGAGCTCGGAGAGGGAGACAA
[G,A]
ATGAACTCTATGAAAGTGCAGTCGAAACTGTATGACACTGACCATGTATGAATTATTACT
ATTACCGTTTCCTGAGAAGGGCCGCACAACCAGCCAATGTAGGCTATTTTATGAGAAATG
AGTCTTAACTGCCACACTCCCCTTATAAATCTCATTCAACTGATGCTGTTAAACAAAGCC
TCTCTGAACAGCCGCTTGCTGGCTCTTTGCCTTGCTCTAATGCATTGGTTCTTTGTCCAT
GTAGAAAGGGAACTATTAGGTTCAACCAGATTCATGAAGCATCCACTCTGTGCCAGGCAC

9537   AACTGATGCTGTTAAACAAAGCCTCTCTGAACAGCCGCTTGCTGGCTCTTTGCCTTGCTC
TAATGCATTGGTTCTTTGTCCATGTAGAAAGGGAACTATTAGGTTCAACCAGATTCATGA
AGCATCCACTCTGTGCCAGGCACCATGCTGGGCCCTGGGAGGAGAGGGGTGACGCTTGTC
CTGCAGGGTTGGAACAGGCAAGGGAGGGAAGACCACATAGCACCAAAGGTCTAGGGGTCT
GTGGACTCGTGAGCATACAGGGTTCAGAATCTGGGAGTTAACAAACGAGGCCCTACCACA
[G,T]
ACTGGCCCGGGGACCTTGGGCAAGTTAGGTTCTCTCAGCCTCAGTTTCCTCCTTTGTAAA
ACAGGAGTGATGGTCCCTACCCTATGGGGTGGTGCTGAGGATTCAGACTGGATGGGATAA
CTTAGGCAAAGATCCCGGCACACCATGGGGGCCTGGCTGGTCCCTGTGGGCTGGTGAAGG
ACTTGGCTGCCCTCCCCACTCACACCCTTGGGTTCTGCCTCCTTCCTGGCTCCTCGGCAG
GTTCCCCACCCCGGTGTCGCCTGTGGTCTCACAGTGGAAGGACATGATAGGCACAGCCTT

12302   AGCCCCACCATAACCTATGGGAGAGGATTTACTAAACTTTCTTAACGGTGATGAAACCAA
GGCTCAGAATGGTTAAGTAAATTGTCAAAGGCCACAGAGGTAGGGAGTGGTAGAGTCTGG
ATTAAAACTCCAAGTCCTGGACTCCAGACCTCTAGGCTGTACTGTCTCATAGGGAAGGCA
GTCTCACCCACCTAGGGCAGAGAAGAAAATCCTTAAAGCCAGAGAAGTGAGTGGCTCATC
TGTGGTCACCCAGAGAGACAGTGATGAGGACAGGGAGAAAAATTATACCTCAGTTCCCAG
[C,G]
CCAAGGATCTGCTTTGACCATAACCCAACAAGCCCCCGCTATGGTGGTATTTCCTTAGGT
TCATATGGCGGCTTTTGTTTCCATTTGATCTTCACAGCAATTCTCTACAGGAATCTGGGC
AGATTTATTTCCTTTAGAGGAATTTCCAGGTCTTAAAATCTATAGGGGGCAACTATCAAA
ACTTCACCCAATGTTGCCCCCTACCCACACACAAAACCAGGCCCCCAGCCGATCAGAAAG
CACTGCTGAGCTCCTGTCAGGGCCCACGCAGCTCGCTGTGAGACAGAGAGAGGGAACTCA

12354   GAAACCAAGGCTCAGAATGGTTAAGTAAATTGTCAAAGGCCACAGAGGTAGGGAGTGGTA
GAGTCTGGATTAAAACTCCAAGTCCTGGACTCCAGACCTCTAGGCTGTACTGTCTCATAG
GGAAGGCAGTCTCACCCACCTAGGGCAGAGAAGAAAATCCTTAAAGCCAGAGAAGTGAGT
GGCTCATCTGTGGTCACCCAGAGAGACAGTGATGAGGACAGGGAGAAAAATTATACCTCA
GTTCCCAGCCCAAGGATCTGCTTTGACCATAACCCAACAAGCCCCCGCTATGGTGGTATT
[C,T]
CCTTAGGTTCATATGGCGGCTTTTGTTTCCATTTGATCTTCACAGCAATTCTCTACAGGA
ATCTGGGCAGATTTATTTCCTTTAGAGGAATTTCCAGGTCTTAAAATCTATAGGGGGCAA
CTATCAAAACTTCACCCAATGTTGCCCCCTACCCACACACAAAACCAGGCCCCCAGCCGA
TCAGAAAGCACTGCTGAGCTCCTGTCAGGGCCCACGCAGCTCGCTGTGAGACAGAGAGAG
GGAACTCACATTTATTGATCACCTACTGAGCATCCATCACTAGGCTAGGACCGTCACATT

12487   ACCCACCTAGGGCAGAGAAGAAAATCCTTAAAGCCAGAGAAGTGAGTGGCTCATCTGTGG
TCACCCAGAGAGACAGTGATGAGGACAGGGAGAAAAATTATACCTCAGTTCCCAGCCCAA
GGATCTGCTTTGACCATAACCCAACAAGCCCCCGCTATGGTGGTATTTCCTTAGGTTCAT
ATGGCGGCTTTTGTTTCCATTTGATCTTCACAGCAATTCTCTACAGGAATCTGGGCAGAT
TTATTTCCTTTAGAGGAATTTCCAGGTCTTAAAATCTATAGGGGGCAACTATCAAAACTT
[C,T]
ACCCAATGTTGCCCCCTACCCACACACAAAACCAGGCCCCCAGCCGATCAGAAAGCACTG
CTGAGCTCCTGTCAGGGCCCACGCAGCTCGCTGTGAGACAGAGAGAGGGAACTCACATTT
ATTGATCACCTACTGAGCATCCATCACTAGGCTAGGACCGTCACATTCCTTAACTTTTGA
ATCCTTTCATGAGGTAGGCATTATTATTCTCCTTTTGTTTCACATAGCCATTAAAGAACA
AAATTTGGGGCTGGGTGTGCTGACTCACACCTGTGATCTAGCACTTTAGGGGGCTGAGGC

13198   CTAACTATTCAGGAAGGTTAGGCGGGAGCACAACTTGGGTTCCAGGGTTTGAGGCTCCAG
TGAGCTGATCTTGCCACTGCACTACAGCCTGAGCAACAGAGCAAGACCCTGTGACTCCAA
AAACAAACAAACAAACACATTTTGAACCCAAACAGATCTGACCCAAGATGCATGCTCTTA

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        TAGATGCCACCTCCCTGTGTGCTGGGGCTTCTACTAAAAACACAGACAAGATCAGGCAAC
        CACAGTCAATCTAAGGGAAAGAGGAAAGTGTAACCAAAGCACAAATACATAAAATATTGC
        [-,A]
        AAAATGCTATTTAAAGAAAAAAAAGAGAAGAGAGGCTCTGAGGTTGTACTAACAGAGAAT
        GGCCTTGGCTAATCCAGGAAGACTTCCTGAAAGAGGTTGTTTTTTCCCCAGGTCTGCTTT
        TGACATCTCTCTTTTCACAGTGCATCTGGGTAGTGAGCTTCCTCTCCTCCTTCTTCCTCA
        GCCTGCCCTATGGTGTGGCAGTGGGTGTCGCCTTCTCCGTCCTGGTCGTGGTCTTCCAGA
        CTCAGTTGTAAGTGATAGCTTCCGCCCTCCTAGGCCCACAGTCGGTTCCCTGGGCCAGCC

13257   GTGAGCTGATCTTGCCACTGCACTACAGCCTGAGCAACAGAGCAAGACCCTGTGACTCCA
        AAAACAAACAAACAAACACATTTTGAACCCAAACAGATCTGACCCAAGATGCATGCTCTT
        ATAGATGCCACCTCCCTGTGTGCTGGGGCTTCTACTAAAAACACAGACAAGATCAGGCAA
        CCACAGTCAATCTAAGGGAAAGAGGAAAGTGTAACCAAAGCACAAATACATAAAATATTG
        CAAAAATGCTATTTAAAGAAAAAAAAGAGAAGAGAGGCTCTGAGGTTGTACTAACAGAGA
        [A,G]
        TGGCCTTGGCTAATCCAGGAAGACTTCCTGAAAGAGGTTGTTTTTTCCCCAGGTCTGCTT
        TTGACATCTCTCTTTTCACAGTGCATCTGGGTAGTGAGCTTCCTCTCCTCCTTCTTCCTC
        AGCCTGCCCTATGGTGTGGCAGTGGGTGTCGCCTTCTCCGTCCTGGTCGTGGTCTTCCAG
        ACTCAGTTGTAAGTGATAGCTTCCGCCCTCCTAGGCCCACAGTCGGTTCCCTGGGCCAGC
        CCGCAAAGGGCTTCCATGCCACGGCCTGGCTTAGTCCACTGTACCTTCCACCTCTGGGCC

14541   TCATGGACACTGACATTTATGTGAATCCCAAGACCTATAATAGGGTAGGTAATTCAAGCT
        TATGACCTCCTTCTTTTGCTCTGCACCACCCCAAGAAGAGGTTGCTTTTTAAAGCCAATA
        AAGACATTTCTGCAACTTGAGCTCAGTCTCCCTGTCACAGGCCCAGGATATCCAGGGGAT
        TAAAATCATCACGTACTGCTCCCCTCTCTACTTTGCCAACTCAGAGATCTTCAGGCAAAA
        GGTCATCGCCAAGGTAAGGCTCAGTCCCTGGCGACCAGAGGCTCTGGACAGAGAGTGGCC
        [G,A]
        GAAAATGGAAGCAGAAGGGCGGTGGGAGCTGAGAATAGGCCACTCCCATAGAGGGTGGAG
        GTCAAGATTGCTGTTGGCTCTCTCCCTGCAGACAGGCATGGACCCCCAGAAAGTATTACT
        AGCCAAGCAAAAATACCTCAAGAAGCAGGAGAAGCGGAGAATGAGGCCCACACAACAGAG
        GAGGTCTCTATTCATGAAAACCAAGGTGAATGAAGGCCAGAAGCAGCCCCGTGCCCTGCT
        CTCCTGCCCATTCTGATACTGCCCCCTGTTACTCATGGTACCCTGGGGGCCCCGCTTCCC

14545   GGACACTGACATTTATGTGAATCCCAAGACCTATAATAGGGTAGGTAATTCAAGCTTATG
        ACCTCCTTCTTTTGCTCTGCACCACCCCAAGAAGAGGTTGCTTTTTAAAGCCAATAAAGA
        CATTTCTGCAACTTGAGCTCAGTCTCCCTGTCACAGGCCCAGGATATCCAGGGGATTAAA
        ATCATCACGTACTGCTCCCCTCTCTACTTTGCCAACTCAGAGATCTTCAGGCAAAAGGTC
        ATCGCCAAGGTAAGGCTCAGTCCCTGGCGACCAGAGGCTCTGGACAGAGAGTGGCCGGAA
        [A,G]
        ATGGAAGCAGAAGGGCGGTGGGAGCTGAGAATAGGCCACTCCCATAGAGGGTGGAGGTCA
        AGATTGCTGTTGGCTCTCTCCCTGCAGACAGGCATGGACCCCCAGAAAGTATTACTAGCC
        AAGCAAAAATACCTCAAGAAGCAGGAGAAGCGGAGAATGAGGCCCACACAACAGAGGAGG
        TCTCTATTCATGAAAACCAAGGTGAATGAAGGCCAGAAGCAGCCCCGTGCCCTGCTCTCC
        TGCCCATTCTGATACTGCCCCCTGTTACTCATGGTACCCTGGGGGCCCCGCTTCCCACCC

15041   ACCAAGGTGAATGAAGGCCAGAAGCAGCCCCGTGCCCTGCTCTCCTGCCCATTCTGATAC
        TGCCCCCTGTTACTCATGGTACCCTGGGGGCCCCGCTTCCCACCCTGACAGGCAAAGACA
        GAAAGTCTCTGGGAACACTGCCTGGTGGCCGCTGGGCATTTTTCTTCTTTTTTTTCTTTT
        TCTTTTTAGAGATGGAATTTTGCTCTTGTCACCCAGGCTTGAGTGCAATGGCGTTATCTT
        GGCTCACTGCAACCTCCACCTCTGGGGTTCAAGCGATTCTCCTGCCTTAGCCTCCCAAGT
        [C,A]
        GCTGAGATTACAGGTGCCACCACACCCAGCTAATTTTTGTATTTTTAGTAGATATTGGGT
        TTCACCATGTTGGCCAGGCTGGTGTCAAACTCCTGACCTCAGGTGATCCACCTACCTTAG
        CCTTCCAAAGTGCTGGGATTACAAGCCTGAGCCACTGCGCCCAGCCTGGGCATTTTTCTT
        CTTGGATGAGGTGCTACCATCTCCCAGGGAAGCCACTGAACCCCCAAGGCCCTTCTCCAT
        TTTCTGGCTAAGATAGGACATGGCCCATGGACTTTTGAACAACCCAGAGGGGGAACAGCA

15053   GAAGGCCAGAAGCAGCCCCGTGCCCTGCTCTCCTGCCCATTCTGATACTGCCCCCTGTTA
        CTCATGGTACCCTGGGGGCCCCGCTTCCCACCCTGACAGGCAAAGACAGAAAGTCTCTGG
        GAACACTGCCTGGTGGCCGCTGGGCATTTTTCTTCTTTTTTTTCTTTTTCTTTTTAGAGA
        TGGAATTTTGCTCTTGTCACCCAGGCTTGAGTGCAATGGCGTTATCTTGGCTCACTGCAA
        CCTCCACCTCTGGGGTTCAAGCGATTCTCCTGCCTTAGCCTCCCAAGTCGCTGAGATTAC
        [A,C]
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       GGTGCCACCACACCCAGCTAATTTTTGTATTTTTAGTAGATATTGGGTTTCACCATGTTG
       GCCAGGCTGGTGTCAAACTCCTGACCTCAGGTGATCCACCTACCTTAGCCTTCCAAAGTG
       CTGGGATTACAAGCCTGAGCCACTGCGCCCAGCCTGGGCATTTTTCTTCTTGGATGAGGT
       GCTACCATCTCCCAGGGAAGCCACTGAACCCCCAAGGCCCTTCTCCATTTTCTGGCTAAG
       ATAGGACATGGCCCATGGACTTTTGAACAACCCAGAGGGGGAACAGCAGTGAATTTCCTG

15065  CAGCCCCGTGCCCTGCTCTCCTGCCCATTCTGATACTGCCCCCTGTTACTCATGGTACCC
       TGGGGGCCCCGCTTCCCACCCTGACAGGCAAAGACAGAAAGTCTCTGGGAACACTGCCTG
       GTGGCCGCTGGGCATTTTTCTTCTTTTTTTTCTTTTTCTTTTTAGAGATGGAATTTTGCT
       CTTGTCACCCAGGCTTGAGTGCAATGGCGTTATCTTGGCTCACTGCAACCTCCACCTCTG
       GGGTTCAAGCGATTCTCCTGCCTTAGCCTCCCAAGTCGCTGAGATTACAGGTGCCACCAC
       [A,G]
       CCCAGCTAATTTTTGTATTTTTAGTAGATATTGGGTTTCACCATGTTGGCCAGGCTGGTG
       TCAAACTCCTGACCTCAGGTGATCCACCTACCTTAGCCTTCCAAAGTGCTGGGATTACAA
       GCCTGAGCCACTGCGCCCAGCCTGGGCATTTTTCTTCTTGGATGAGGTGCTACCATCTCC
       CAGGGAAGCCACTGAACCCCCAAGGCCCTTCTCCATTTTCTGGCTAAGATAGGACATGGC
       CCATGGACTTTTGAACAACCCAGAGGGGGAACAGCAGTGAATTTCCTGGGGAACCCAGGC

15108  TGTTACTCATGGTACCCTGGGGGCCCCGCTTCCCACCCTGACAGGCAAAGACAGAAAGTC
       TCTGGGAACACTGCCTGGTGGCCGCTGGGCATTTTTCTTCTTTTTTTTCTTTTTCTTTTT
       AGAGATGGAATTTTGCTCTTGTCACCCAGGCTTGAGTGCAATGGCGTTATCTTGGCTCAC
       TGCAACCTCCACCTCTGGGGTTCAAGCGATTCTCCTGCCTTAGCCTCCCAAGTCGCTGAG
       ATTACAGGTGCCACCACACCCAGCTAATTTTTGTATTTTTAGTAGATATTGGGTTTCACC
       [A,C]
       TGTTGGCCAGGCTGGTGTCAAACTCCTGACCTCAGGTGATCCACCTACCTTAGCCTTCCA
       AAGTGCTGGGATTACAAGCCTGAGCCACTGCGCCCAGCCTGGGCATTTTTCTTCTTGGAT
       GAGGTGCTACCATCTCCCAGGGAAGCCACTGAACCCCCAAGGCCCTTCTCCATTTTCTGG
       CTAAGATAGGACATGGCCCATGGACTTTTGAACAACCCAGAGGGGGAACAGCAGTGAATT
       TCCTGGGGAACCCAGGCAGCCCAGGGCTAGCAAGGCTGGGGTGGCCATGGCAGTAATCCT

16274  CTTCCAGACTGTCTCCCTGCAGGAGCTGCAGCAGGACTTTGAGAATGCGCCCCCCACCGA
       CCCCAACAACAACCAGACCCCGGCTAACGGCACCAGCGTGTCCTATATCACCTTCAGCCC
       TGACAGCTCCTCACCTGCCCAGAGTGAGCCACCAGCCTCCGCTGAGGCCCCCGGCGAGCC
       CAGTGACATGCTGGCCAGCGTCCCACCCTTCGTCACCTTCCACACCCTCATCCTGGACAT
       GAGTGGAGTCAGCTTCGTGGACTTGATGGGCATCAAGGCCCTGGCCAAGGTGAGGCCCTC
       [-,G]
       GGGACAGCAAGCACCACCCACTCCACCCCCTCCGCTCTGCTCTCCACATTCCCTTTCCTG
       GGAGCCCTCATTTCAGGAAGCTGAGGGAGGAAGCTCACTGGGGAGACTAACAGCTCCTAG
       GAATCCCTCCTTTCCCCAGACGCCACCAGGTTGAGACATTCTCCACAGAGCAGGCCCAGA
       CGGCCCATGACAATGAGTGGCGGGACAAGTCTACCAGAGTTTCAGGCCCCTGTGCTCCCA
       ACACCCCCAGCAGTGGCCATCCCAAGTCCCTCTCAGCCATCAGGAACCCACCCAGGTTCT

17424  AACATGGTGAAACCCCGCCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGACGGGC
       CCCTGTAGTCCCAGCTACTCGGTAGGCTGAGGCAGAGAATTGCTTGAACCCAGGAGGCGG
       AGGTTGCAGTGAGCCAAGATCGCGCCACTGCACTCCAGCCTGGGCAACAGAGTGAAACTC
       CATCTCAAAAGAAAAAAAAAGAAAATATCTAGCCCCACAAGAAGGGGCCATGGTGACTTT
       AAGTGCCCGCCACGTTGGCAAAAGTCCATTTCCGCTCCACTTCCCAGAGAAACCGTCAGC
       [C,T]
       AACACTCCAGGGAGAAGTGGTGTGCTTTGCTGCTATTTTTGTCTTTGGCTGCTGGGCTCT
       CAGGGTTGCTTATTTGTTTGGCTTCCCCTCTGAAGTACGTTTTGTGAATCACTTTTGAGA
       CCCACTCAGAACATTCCTTTCCTTTTGCCTCCCTACCCCAACAACACTTCTAGCTGAGCT
       CCACCTATGGGAAGATCGGCGTGAAGGTCTTCTTGGTGAACATCCATGGTAAGAGAAAGA
       GGACATTTAGGGACTGAAAGACTGGCAAGGAGTGTGGGGTAGGAACAGGTTGGTGGGGTC

17627  AATATCTAGCCCCACAAGAAGGGGCCATGGTGACTTTAAGTGCCCGCCACGTTGGCAAAA
       GTCCATTTCCGCTCCACTTCCCAGAGAAACCGTCAGCCAACACTCCAGGGAGAAGTGGTG
       TGCTTTGCTGCTATTTTTGTCTTTGGCTGCTGGGCTCTCAGGGTTGCTTATTTGTTTGGC
       TTCCCCTCTGAAGTACGTTTTGTGAATCACTTTTGAGACCCACTCAGAACATTCCTTTCC
       TTTTGCCTCCCTACCCCAACAACACTTCTAGCTGAGCTCCACCTATGGGAAGATCGGCGT
       [G,A]
       AAGGTCTTCTTGGTGAACATCCATGGTAAGAGAAAGAGGACATTTAGGGACTGAAAGACT
       GGCAAGGAGTGTGGGGTAGGAACAGGTTGGTGGGGTCTGAATAGTGAGGAGGTTGGAAAC
       GAGAGCACCCAGCTATCCCCCACAAGCTGCTGCCTGCTCATAAAAGCTTCAGGTACAAGT
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FIGURE 3, page 16 of 20

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                CCAAAGAGACTGGTCAGATTGCATAAACATCCTAGGGGCCTTAGTGACAGAGTGGGGGTG
                AGGAGGTCATGGAGTTACAGAAGGACAGCTAGGATTCTAATCTACCCCATAACTAATTTG

     18427      GGGTGCATATACACAGCCTCAAGGACGTGGCCACAGGGCAGCAGACATTTACATGACTAG
                CATGTACGCAAAGTGCAGAGATGTGGGAGCAAGTGCACACAGACACACAGGAGAATGTGA
                AGGGGCACATACACACACACCCAGCTCCCTGCACTGGGTCAGACCCCCTCCAGCAGGGCT
                GCAGTTCCCAAGCTCCGCATGGCCACGTTCGGGGAGAGAATCTGCAGTGGCAATGACCTG
                CTATGATATGTTCTGGAGTTAGAAGCAGTGGATTCTCCCCAACCTCACTGGACACCCCCT
                [T,C]
                AGGAAACCATCTCTAGGATTAAGAGTAATCCACACAAACTTCCAATGCCACACATTGGAA
                GTTGCTGGAAAGGTCTGGGAAAACAAGAGGAAGGATGGGTCCTTGGGGGATAGAACTGGC
                AGCGGCCTCTTCAAGGATGGCTTAGGCTTTTCCACTCGAATCACCACAAAGTACTGACTC
                CCTAAATCAAACTGCTTCCTTCTGCTCTGGGTTGAAACTTCAGCATCCTCAAGTTCATGT
                TGCCCTCTGCCGTCCAGAACTGATATTGCACTGCCAATGCCATGGCCCTCAGATACAGCA

     18813      AGAGGAAGGATGGGTCCTTGGGGGATAGAACTGGCAGCGGCCTCTTCAAGGATGGCTTAG
                GCTTTTCCACTCGAATCACCACAAAGTACTGACTCCCTAAATCAAACTGCTTCCTTCTGC
                TCTGGGTTGAAACTTCAGCATCCTCAAGTTCATGTTGCCCTCTGCCGTCCAGAACTGATA
                TTGCACTGCCAATGCCATGGCCCTCAGATACAGCAAGAGCTGGGACCTCAGGCCTCTCCC
                ATCCCTGCTCTGGTCTCACTATCTTCCCCACCCCCAGCTCCAATCCACAATGGCTGTTAT
                [C,G]
                TTTCTGAAGGTGATCTTTTCTCCTTCTAGCCCAGGTGTACAATGACATTAGCCATGGAGG
                CGTCTTTGAGGATGGGAGTCTAGAATGCAAGCACGTCTTTCCCAGCATACATGACGCAGT
                CCTCTTTGCCCAGGCAAATGCTAGAGACGTGACCCCAGGACACAACTTCCAAGGGGTAAG
                GTTCTTGCACCTGGGGAATCCTAGGCTCCAAGGCACTGAAATAGCAGGACCAAGAGGCAT
                TATTAGAAAGAACACAGGAGAAGGTTTAAGTTCCAATATCAAGTCTGCCATTTCAGTTTT

     19035      GGACCTCAGGCCTCTCCCATCCCTGCTCTGGTCTCACTATCTTCCCCACCCCCAGCTCCA
                ATCCACAATGGCTGTTATCTTTCTGAAGGTGATCTTTTCTCCTTCTAGCCCAGGTGTACA
                ATGACATTAGCCATGGAGGCGTCTTTGAGGATGGGAGTCTAGAATGCAAGCACGTCTTTC
                CCAGCATACATGACGCAGTCCTCTTTGCCCAGGCAAATGCTAGAGACGTGACCCCAGGAC
                ACAACTTCCAAGGGGTAAGGTTCTTGCACCTGGGGAATCCTAGGCTCCAAGGCACTGAAA
                [T,C]
                AGCAGGACCAAGAGGCATTATTAGAAAGAACACAGGAGAAGGTTTAAGTTCCAATATCAA
                GTCTGCCATTTCAGTTTTCTGAATCTGTTTCCTTATCTATAGAATGAGCACCATCAACTA
                ACATTACCTACCTCTCTGCATTTTTCTTTTATTTTGTTTTAGGGTTAAATGATAATTACA
                TCTTTTGTGTCACTTGAAAGCACTTTGTGTATTGTAAAAATTCTTTATCAATATAAGTTT
                TCTGGTTGCACAAACACCCAAAGCATAGTAGAGCAGGCCCACTCTGCTGGCATCGTTCCC

     19182      AGGATGGGAGTCTAGAATGCAAGCACGTCTTTCCCAGCATACATGACGCAGTCCTCTTTG
                CCCAGGCAAATGCTAGAGACGTGACCCCAGGACACAACTTCCAAGGGGTAAGGTTCTTGC
                ACCTGGGGAATCCTAGGCTCCAAGGCACTGAAATAGCAGGACCAAGAGGCATTATTAGAA
                AGAACACAGGAGAAGGTTTAAGTTCCAATATCAAGTCTGCCATTTCAGTTTTCTGAATCT
                GTTTCCTTATCTATAGAATGAGCACCATCAACTAACATTACCTACCTCTCTGCATTTTTC
                [T,C]
                TTTATTTTGTTTTAGGGTTAAATGATAATTACATCTTTTGTGTCACTTGAAAGCACTTTG
                TGTATTGTAAAAATTCTTTATCAATATAAGTTTTCTGGTTGCACAAACACCCAAAGCATA
                GTAGAGCAGGCCCACTCTGCTGGCATCGTTCCCTGCCTCCTCCTCATCTCTTTCTAAAGG
                GGGCTTTCGGGAAGGGAGGGGAGGGGAGTAAGCCTACCCATTTTAACTTACCGGAGCTTA
                GAGATTTCAGGCTGGTGAGGGATAAAGAGATTGGGTCTGAGTTTTGTCTCAGCTTTTTGA

     19508      TAATTACATCTTTTGTGTCACTTGAAAGCACTTTGTGTATTGTAAAAATTCTTTATCAAT
                ATAAGTTTTCTGGTTGCACAAACACCCAAAGCATAGTAGAGCAGGCCCACTCTGCTGGCA
                TCGTTCCCTGCCTCCTCCTCATCTCTTTCTAAAGGGGGCTTTCGGGAAGGGAGGGGAGGG
                GAGTAAGCCTACCCATTTTAACTTACCGGAGCTTAGAGATTTCAGGCTGGTGAGGGATAA
                AGAGATTGGGTCTGAGTTTTGTCTCAGCTTTTTGACATTTAATTTACTAGCTCAGTAAGT
                [-,G,C]
                ATACAAATGGGATACAAATAACACCATCTAAAACTCCAGAAGACTGGGGAGTCAGAAAAA
                TCCTACCTCCTTGGGGTCCCTGCCCAGATCCCCAGTCATCTCTAGCCCTCAGGGTCCCCT
                CCCAGCTCAGCTCCTGCCCTTGGCCTCCCAAGACTCTTGTTGTGCCCCAGCCCTGGGTAA
                AAACCTCCCCTGCCCTCTGTGGGTCATAAGAAAGGCTTTTCTGGCCCTAGAGCAATGATT
                TGCTCTTTGCCTTAAGAGACTGATGAAGGTGAAACCATCTGTTCTAAGTGCTGAAAGACT
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<div align="center">FIGURE 3, page 17 of 20</div>

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19571   AGTTTTCTGGTTGCACAAACACCCAAAGCATAGTAGAGCAGGCCCACTCTGCTGGCATCG
        TTCCCTGCCTCCTCCTCATCTCTTTCTAAAGGGGGCTTTCGGGAAGGGAGGGGAGGGGAG
        TAAGCCTACCCATTTTAACTTACCGGAGCTTAGAGATTTCAGGCTGGTGAGGGATAAAGA
        GATTGGGTCTGAGTTTTGTCTCAGCTTTTTGACATTTAATTTACTAGCTCAGTAAGTCAT
        ACAAATGGGATACAAATAACACCATCTAAAACTCCAGAAGACTGGGGAGTCAGAAAAATC
        [T,G,C]
        TACCTCCTTGGGGTCCCTGCCCAGATCCCCAGTCATCTCTAGCCCTCAGGGTCCCCTCCC
        AGCTCAGCTCCTGCCCTTGGCCTCCCAAGACTCTTGTTGTGCCCCAGCCCTGGGTAAAAA
        CCTCCCCTGCCCTCTGTGGGTCATAAGAAAGGCTTTTCTGGCCCTAGAGCAATGATTTGC
        TCTTTGCCTTAAGAGACTGATGAAGGTGAAACCATCTGTTCTAAGTGCTGAAAGACTGCC
        CAGGAACACACAGGGCGCTGGCTCCTGCCCTCCATGCCTAGAGGGAAACCCTGGGGAAAC

20147   GCCTAGAGGGAAACCCTGGGGAAACAACGGGCTTTCCTGCTTCGTGAAATTTGTCCGCAG
        AGCAAAGAGGGAGATTCTGGAGGAAGCTGCATTAGTTGTTAGTGCCCTAATCATGTTCAG
        CTACTCTAGTTGGTATGTATACTTGATTAGTCATAGCACTTATAAATAATTTATATTTTA
        TATAATATATACTTACATATTATAGACCATTCACAGATACAAATCACACACATAAACACA
        CACCTTTTCAACAGCATTGTGAGGGACAAAGCAGGCAAAGTGAGGCTGGTTATCAGACTT
        [T,G]
        AACAGATTAGAAAATATATTCCCAGGAGGACAGGAATTCCCCAAGGTCAGGCAGCTAGCC
        AATAGTTTTTCTAAGCTGAGTAAAACCTTCCCTGCCTCTAACGGCCCACAAAGGAGGGAA
        GACCGCGATACACACCTGTCTGGTATAAGGGGGAAGACCACAGCCGTGCTGTTTTTGTGA
        GGCAGGTAAGGGAAGGGGCAAGAGGATAAGTCATGTGTCAGGAAGCAGCGTCCAACCAGA
        GCCGGCCACCTGTCCCTTTTCCTGCCACCATGCACCAACTTTGCTGTTCAGTCACTGAAG

20180   TTCCTGCTTCGTGAAATTTGTCCGCAGAGCAAAGAGGGAGATTCTGGAGGAAGCTGCATT
        AGTTGTTAGTGCCCTAATCATGTTCAGCTACTCTAGTTGGTATGTATACTTGATTAGTCA
        TAGCACTTATAAATAATTTATATTTTATATAATATATACTTACATATTATAGACCATTCA
        CAGATACAAATCACACACATAAACACACACCTTTTCAACAGCATTGTGAGGGACAAAGCA
        GGCAAAGTGAGGCTGGTTATCAGACTTTAACAGATTAGAAAATATATTCCCAGGAGGACA
        [G,A]
        GAATTCCCCAAGGTCAGGCAGCTAGCCAATAGTTTTTCTAAGCTGAGTAAAACCTTCCCT
        GCCTCTAACGGCCCACAAAGGAGGGAAGACCGCGATACACACCTGTCTGGTATAAGGGGG
        AAGACCACAGCCGTGCTGTTTTTGTGAGGCAGGTAAGGGAAGGGGCAAGAGGATAAGTCA
        TGTGTCAGGAAGCAGCGTCCAACCAGAGCCGGCCACCTGTCCCTTTTCCTGCCACCATGC
        ACCAACTTTGCTGTTCAGTCACTGAAGCTCATTCTGCACTGGCTTCCTCCCTTCCAGGCT

20584   TGTCTGGTATAAGGGGGAAGACCACAGCCGTGCTGTTTTTGTGAGGCAGGTAAGGGAAGG
        GGCAAGAGGATAAGTCATGTGTCAGGAAGCAGCGTCCAACCAGAGCCGGCCACCTGTCCC
        TTTTCCTGCCACCATGCACCAACTTTGCTGTTCAGTCACTGAAGCTCATTCTGCACTGGC
        TTCCTCCCTTCCAGGCTCCAGGGGATGCTGAGCTCTCCTTGTACGACTCAGAGGAGGACA
        TTCGCAGCTACTGGGACTTAGAGCAGGTGAGCTGAGGGAAGGGGCTGTGAGGGTGGGAGC
        [A,T]
        GGGCGAAGAGGGGAAGGATGGGGTCGCTGTCAAATACAAGGCGTTCACTCAGCTGTCTCA
        CCTCCAGCCCAGAGCAGTCACATTCAAGGCCACAAAGATTTGTGGTCATCTTTGTTTTTT
        TTCTTTTTCCTTTTCTTTTTTTTTTTTTTTTTAATTTGAGACAAAGTCTCACTCTATCACCC
        AGACTGGAATGCAGTGGCATGATCTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCCAGA
        GGTTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTTCAGGCCTGCGCCCAGCTAATTTT

20717   ATGCACCAACTTTGCTGTTCAGTCACTGAAGCTCATTCTGCACTGGCTTCCTCCCTTCCA
        GGCTCCAGGGGATGCTGAGCTCTCCTTGTACGACTCAGAGGAGGACATTCGCAGCTACTG
        GGACTTAGAGCAGGTGAGCTGAGGGAAGGGGCTGTGAGGGTGGGAGCAGGGCGAAGAGGG
        GAAGGATGGGGTCGCTGTCAAATACAAGGCGTTCACTCAGCTGTCTCACCTCCAGCCCAG
        AGCAGTCACATTCAAGGCCACAAAGATTTGTGGTCATCTTTGTTTTTTTTCTTTTCCTTT
        [T,C]
        CTTTTTTTTTTTTTTTTTTAATTTGAGACAAAGTCTCACTCTATCACCCAGACTGGAATGCA
        GTGGCATGATCTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCCAGAGGTTCTCCTGCCT
        CAGCCTCCCGAGTAGCTGGGACTTCAGGCCTGCGCCCAGCTAATTTTTGTATTTTTAGTA
        GAGACAGCTTTTCACCATGTTGGCTGGGCTGGTCTCGAACTTCCGATCTCAAGCAATCTG
        CCTGCCTCGGTCTCCTAAGTGCCTGGATTACAGGCATAAGCCACGATGCCTGGCCTTTGT

20894   GGGGAAGGATGGGGTCGCTGTCAAATACAAGGCGTTCACTCAGCTGTCTCACCTCCAGCC
        CAGAGCAGTCACATTCAAGGCCACAAAGATTTGTGGTCATCTTTGTTTTTTTTTCTTTTCC
        TTTTCTTTTTTTTTTTTTTTTTAATTTGAGACAAAGTCTCACTCTATCACCCAGACTGGAA
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TGCAGTGGCATGATCTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCCAGAGGTTCTCCT
GCCTCAGCCTCCCGAGTAGCTGGGACTTCAGGCCTGCGCCCAGCTAATTTTTGTATTTTT
[A,G]
GTAGAGACAGCTTTTCACCATGTTGGCTGGGCTGGTCTCGAACTTCCGATCTCAAGCAAT
CTGCCTGCCTCGGTCTCCTAAGTGCCTGGATTACAGGCATAAGCCACGATGCCTGGCCTT
TGTTTTCATTCTTCTCACTCCCTGAAAGGCATCGTGGGGAGAGGGTGAGTCACTGGACCA
AGTCCTAGAGAACCAGTATCTATTCTTATTCTCCAACACATCACCCACGTGACCCTGAGC
AAGCCACATACACCCTGGGCCCTAGTTTTTATCATCTGTGAAATTAGGGGAAACATAGGT

21787   GGGTGCAATGGTTCACACCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGCGGACCAC
         CTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCGTCTCTACTAAAA
         GCACAAAAATTAGCCAGGCGTAGTGGTGCATGCCTGTAGTCCCAGCTACTCGGAAGTCTG
         AGGCATGAGAATCACTTGAACCTGGGAGGCAGATGTTGCAGTGAGCCGAGATCGTGCCAC
         TGCACTCCAGCTTGGGTGACAGAGCTAGACTGTCTCAAAAACAAACAAACAAAACAAAAC
         [-,A,C]
         TAAAAGATATGTGGATATGAGGGATCACCATCCCCATAGGGCCCCTGGATTAACACCACC
         CCACCAATGCCCTGAATTAAAAGAAACCAGATGACTAGGTTTGGAGAAATCTGGCTTTGG
         GTCTATGAGAAGTAGTGTCTCTCTTTGTGCCTCTTCCCATTCTTTTTGACATTGAGCTCC
         ATGGTGCTCTGAATCCGTCTCTCACAGTGCTGATGGCAGGTGGGACAGATTAGAAAATAG
         AGCTGGAGCCACAGAGATTTGGCAGACTGATTTCGGTGCCCTCTTGGAATCTCCAGCACA

22264   CTCCATGGTGCTCTGAATCCGTCTCTCACAGTGCTGATGGCAGGTGGGACAGATTAGAAA
         ATAGAGCTGGAGCCACAGAGATTTGGCAGACTGATTTCGGTGCCCTCTTGGAATCTCCAG
         CACATTCCAAAAAGCCTGGATAGGACCAAAATAGCTTATCAACGTGAGAAAGGACTTCAG
         AGCTTGTCTACTGCCAACCCTCATTTTACCCAATGAGGAAAGTGAAGCTATTAGGGGGCG
         AGGGACACGTGGAAGGTCACACAGCACACAGGAGGTGATTCACATGTAGATTTCAGCACC
         [T,C]
         GCTCCTGCCACGCTGGACTGGTTCACCTCCTAGGCTGACCCTGCCTCTCCCCTGTTCACA
         CACACTCTCGCACACACACACACACACACACACACACACAGGTGCTTTGTTCTGGCCAGG
         GGTTCCTAGGGTCACCTCTTGGTTGCAGCCACTGTGACCCCAACTGGTCTAACCTCTCTC
         TTCCCCTCCCACTTCCTTCCTGTGGTTCCTGCAGGAGATGTTCGGGAGCATGTTTCACGC
         AGAGACCCTGACCGCCCTGTGAGGGCTCAGCCAGTCCTCATGCTGCCTACAGAGTGCCTG

22338   ACAGAGATTTGGCAGACTGATTTCGGTGCCCTCTTGGAATCTCCAGCACATTCCAAAAAG
         CCTGGATAGGACCAAAATAGCTTATCAACGTGAGAAAGGACTTCAGAGCTTGTCTACTGC
         CAACCCTCATTTTACCCAATGAGGAAAGTGAAGCTATTAGGGGGCGAGGGACACGTGGAA
         GGTCACACAGCACACAGGAGGTGATTCACATGTAGATTTCAGCACCTGCTCCTGCCACGC
         TGGACTGGTTCACCTCCTAGGCTGACCCTGCCTCTCCCCTGTTCACACACACTCTCGCAC
         [-,C,A]
         CACACACACACACACACACACACAGGTGCTTTGTTCTGGCCAGGGGGTTCCTAGGGTCA
         CCTCTTGGTTGCAGCCACTGTGACCCCAACTGGTCTAACCTCTCTCTTCCCCTCCCACTT
         CCTTCCTGTGGTTCCTGCAGGAGATGTTCGGGAGCATGTTTCACGCAGAGACCCTGACCG
         CCCTGTGAGGGCTCAGCCAGTCCTCATGCTGCCTACAGAGTGCCTGGCACTTGGGACTTC
         CATAAAGGATGAGCCTGGGGTCACAGGGGGTGTCGGGCGGAGGAAAGTGCATCCCCCAGA

23363   CAGGGACCATGTGCTCTCCACACCCAGGAGTCTAGGCCTTGGTAACTATGCGCCCCCCGT
         CCATCATCCCCAAGGCTGCCCAAACCACCACTGCTGTCAGCAAGCACATCAGACTCTAGC
         CTGGACAGTGGCCAGGACCGTCGAGACCACCAGAGCTACCTCCCCGGGGACAGCCCACTA
         AGGTTCTGCCTCAGCCTCCTGAAACATCACTGCCCTCAGAGGCTGCTCCCTTCCCCTGGA
         GGCTGGCTAGAAACCCCAAAGAGGGGGATGGGTAGCTGGCAGAATCATCTGGCATCCTAG
         [T,C]
         AATAGATACCAGTTATTCTGCACAAAACTTTTGGGAATTCCTCTTTGCACCCAGAGACTC
         AGAGGGGAAGAGGGTGCTAGTACCAACACAGGGAAAACGGATGGGACCTGGGCCCAGACA
         GTCCCCCTTGACCCCAGGGCCCATCAGGGAAATGCCTCCCTTTGGTAAATCTGCCTTATC
         CTTCTTTACCTGGCAAAGAGCCAATCATGTTAACTCTTCCTTATCAGCCTGTGGCCCAGA
         GACACAATGGGGTCCTTCTGTAGGCAAAGGTGGAAGTCCTCCAGGGATCCGCTACATCCC

23688   AAACTTTTGGGAATTCCTCTTTGCACCCAGAGACTCAGAGGGGAAGAGGGTGCTAGTACC
         AACACAGGGAAAACGGATGGGACCTGGGCCCAGACAGTCCCCCTTGACCCCAGGGCCCAT
         CAGGGAAATGCCTCCCTTTGGTAAATCTGCCTTATCCTTCTTTACCTGGCAAAGAGCCAA
         TCATGTTAACTCTTCCTTATCAGCCTGTGGCCCAGAGACACAATGGGGTCCTTCTGTAGG
         CAAAGGTGGAAGTCCTCCAGGGATCCGCTACATCCCCTAACTGCATGCAGATGTGGAAAG
         [G,A]

GGCTGATCCAGATTGGGTCTTCCTGCACAGGAAGACTCTTTAACACCCTTAGGACCTCAG
GCCATCTTCTCCTATGAAGATGAAAATAGGGGTTAAGTTTTCCATATGTACAAGGAGGTA
TTGAGAGGAACCCTACTGTTGACTTGAAAATAAATAGGTTCCATGTGTAAGTGTTTTGTA
AAATTTCAGTGGAAATGCACAGAAAATCTTCTGGCCTCTCATCACTGCTTTTCTCAAGCT
TCTTCAGCTTAACAACCCCTTCCCTAACAGGTTGGGCTGGCCCAGCCTAGGAAAACATCC

24210   TCACTGCTTTTCTCAAGCTTCTTCAGCTTAACAACCCCTTCCCTAACAGGTTGGGCTGGC
          CCAGCCTAGGAAAACATCCCCCATTTCTAACTTCAGCCAGACCTGCGTTGTGTGTCTGTGT
          GTTGAGTGAGCTGGTCAGCTAACAAGTCTTCTTAGAGTTAAAGGAGGGGGTGCTGGCCAA
          GAGCCAACACATTCTTGGCCCAGGAGCATTGCTTTTCTGTGAATTCATTATGCCATCTGG
          CTGCCAATGGAACTCAAAACTTGGAAGGCGAAGGACAATGTTATCTGGGATTCACCGTGC
          [A,C]
          CAGCACCCGAAGTGCCAAATTCCAGGAGGACAAGAGCCTTAGCCAATGACAACTCACTCT
          CCCCTACTCCACCTCCTTCCAAGTCCAGCTCAGGCCCAGGAGGTGGGAGAAGGTCACAGA
          GCCTCAGGAATTTCCAAGTCAGAGTCCCCTTTGAACCAAGTATCTAGATCCCCTGAGGAC
          TTGATGAAGTGATCCTTAACCCCCAAGTAATCATTAACCCCCAGACCAGCCTCAGAACTG
          AAGGAGATTGTTGACCCAGTGACCTGGAGTTGAGGCTCAGGGAGAGATCTGCCACATGTC

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